

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 14, 2006, 13:05:53 ; Search time 190 Seconds  
(without alignments)  
27.750 Million cell updates/sec

Title: US-09-991-809-1  
Perfect score: 56  
Sequence: 1 KALVQOMQLRQ 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_21:.\*  
1: Geneseqp1980s:.\*  
2: Geneseqp1990s:.\*  
3: Geneseqp2000s:.\*  
4: Geneseqp2001s:.\*  
5: Geneseqp2002s:.\*  
6: Geneseqp2003as:.\*  
7: Geneseqp2003bs:.\*  
8: Geneseqp2004s:.\*  
9: Geneseqp2005s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	12	8 ADE52383	Human apo
2	56	100.0	194	2 AAR39483	Human apo
3	56	100.0	328	2 AAR39484	Human apo
4	56	100.0	333	2 AAR39488	Human apo
5	56	100.0	333	2 AAR39481	Human apo
6	56	100.0	333	2 AAR39497	Human apo
7	56	100.0	333	2 AAR39490	Human apo
8	56	100.0	337	2 AAR39485	Human apo
9	56	100.0	337	2 AAR39492	Human apo
10	56	100.0	337	2 AAR39494	Human apo
11	56	100.0	342	2 AAR39487	Human apo
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13	56	100.0	342	2 AAR39489	Human apo
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15	56	100.0	346	2 AAR39493	Human apo
16	56	100.0	363	2 AAR39478	Human apo
17	56	100.0	363	2 AAR39479	Human apo
18	56	100.0	373	2 AAR39486	Human apo
19	56	100.0	377	2 AAR39502	Human apo
20	56	100.0	377	2 AAR39443	Human apo
21	56	100.0	377	2 AAR45244	Human apo
22	56	100.0	377	2 AAR39501	Human apo
23	56	100.0	377	2 AAR45242	Human apo
24	56	100.0	377	2 AAR39480	Human apo

25	56	100.0	377	2 AAR39499	Human apo
26	56	100.0	377	2 AAR39500	Human apo
27	56	100.0	377	2 AAR45243	Human apo
28	56	100.0	396	4 AAB90664	Human sec
29	56	100.0	396	7 ADE60278	Human Pro
30	56	100.0	396	8 ADQ39968	Human myo
31	56	100.0	401	9 AEA17427	Baboon Ap
32	56	100.0	401	9 AEA17424	Olive bab
33	56	100.0	429	9 AEA17425	Crab-eati
34	51	91.1	28	2 AAR82729	Human apo
35	51	91.1	28	2 AAW70713	Human apo
36	51	91.1	91	9 AEA17426	Chimpanze
37	51	91.1	396	5 AAO15885	Human apo
38	51	91.1	396	5 AAU10862	Human apo
39	51	91.1	396	5 AAU10863	Human apo
40	51	91.1	396	5 AAU10865	Human apo
41	51	91.1	396	5 AAU10867	Human apo
42	51	91.1	396	5 AAU10866	Human apo
43	51	91.1	396	5 AAU10869	Human apo
44	51	91.1	396	5 AAU10861	Human apo
45	51	91.1	396	5 AAU10868	Human apo

ALIGNMENTS

RESULT 1  
ADE52383  
ID ADE52383 standard; peptide; 12 AA.  
XX AC ADE52383;  
XX DT 29-JAN-2004 (first entry)  
XX DE Human apolipoprotein biopolymer marker #1.  
XX KW human; apolipoprotein biopolymer marker; disease state regulation;  
XX KW therapeutic avenue.  
XX OS Homo sapiens.  
XX PN US2003100014-A1.  
XX PD 29-MAY-2003.  
XX PF 23-NOV-2001; 2001US-00991809.  
XX PR 23-NOV-2001; 2001US-00991809.  
XX PA (JACK/) JACKOWSKI G.  
XX PA (MARS/) MARSHALL J.  
XX PI Jackowski G, Marshall J;  
XX WPI; 2004-031198/03.  
XX DR New apolipoprotein biopolymer marker useful for indicating at least one particular disease state, such as, Type II diabetes, using e.g. mass spectrometric analysis.  
XX PT Claim 1; Page 11; 17pp; English.  
XX PS The invention relates to an apolipoprotein biopolymer marker or its analyte useful in indicating a particular disease state. The apolipoprotein biopolymer marker is useful for regulating a disease state by controlling the presence or absence of apolipoprotein biopolymer marker. The apolipoprotein biopolymer marker or a diagnostic kit is useful for identifying therapeutic avenues related to a disease state, which involves conducting an analysis by using the diagnostic kit and interacting with apolipoprotein biopolymer marker. The present sequence represents the amino acid sequence of a human apolipoprotein biopolymer marker.



CC mediates inverse transport of cholesterol. The invention covers  
 CC polypeptides which are derived from apoAIV by deletion of at least 10  
 CC terminal amino acids, by deletion of a helix or pair of helices, by  
 CC addition of a heterologous polypeptide portion or by a point mutation.  
 CC Such muteins are useful in the design of hypocholesterolaemic drugs to  
 CC treat hypercholesterolaemia and atherosclerosis. AAR39484 is a  
 CC specifically claimed mutein and the sequence has been compiled from the  
 CC wild-type sequence (see AAR39443) and the description given in the  
 CC disclosure; the mutant sequence is not shown in the specification.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 328 AA;

Query Match 100.0%; Score 56; DB 2; Length 328;  
 Best Local Similarity 100.0%; Pred. No. 0.22;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KALVQOMEQLRQ 12  
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 DB 248 KALVQOMEQLRQ 259

RESULT 4  
 AAR39488  
 ID AAR39488 standard; protein; 333 AA.

XX AAR39488;

XX 25-MAR-2003 (revised)  
 DT 28-JAN-1994 (first entry)

DE Human apoAIV mutein P(delta h7-8) .

KW apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;  
 KW coronary disease; chylomicron; cholesterol transport; plaque deposition;  
 KW lecithin-cholesterol-acyltransferase; LCAT.

OS Synthetic.

Key Location/Qualifiers  
 Region 14..40  
 Region /note= "helix 1"  
 Region 41..62  
 Region /note= "helix 2"  
 Region 63..95  
 Region /note= "helix 3"  
 Region 96..117  
 Region /note= "helix 4"  
 Region 118..139  
 Region /note= "helix 5"  
 Region 140..161  
 Region /note= "helix 6"  
 Region /note= "helices 7-8 have been deleted from between these two sites"

Region 162..183  
 Region /note= "helix 9"  
 Region 184..205  
 Region /note= "helix 10"  
 Region 206..223  
 Region /note= "helix 11"  
 Region 224..245  
 Region /note= "helix 12"  
 Region 246..267  
 Region /note= "helix 13"  
 Region 268..289  
 Region /note= "helix 14"  
 Region 290..333  
 Region /note= "helix 15"

XX WO315198-A1.

XX 05-AUG-1993.

XX 26-JAN-1993; 93WO-FR000073.  
 XX 27-JAN-1992; 92FR-00000806.  
 XX (RHON ) RHONE POULENC RORER SA.  
 XX Deneffe P, Guinet F, Latta M, Murry-Brellier A;  
 XX WPI; 1993-258676/32.  
 XX New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug design  
 XX and/or treatment of hypercholesterolaemia.  
 XX Claim 7; Page 31-32 and Page 4; 42pp; French.  
 XX Human apolipoprotein AIV is a major component of chylomicrons in lymph  
 XX but is mainly found in the plasma in unassociated form. The apoAIV  
 XX mediates inverse transport of cholesterol. The invention covers  
 XX polypeptides which are derived from apoAIV by deletion of at least 10  
 XX terminal amino acids, by deletion of a helix or pair of helices, by  
 XX addition of a heterologous polypeptide portion or by a point mutation.  
 XX Such muteins are useful in the design of hypocholesterolaemic drugs to  
 XX treat hypercholesterolaemia and atherosclerosis. AAR39488 is a  
 XX specifically claimed mutein and the sequence has been compiled from the  
 XX wild-type sequence (see AAR39443) and the description given in the  
 XX disclosure; the mutant sequence is not shown in the specification.  
 XX (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 333 AA;

Query Match 100.0%; Score 56; DB 2; Length 333;  
 Best Local Similarity 100.0%; Pred. No. 0.22;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KALVQOMEQLRQ 12  
 |||||  
 DB 253 KALVQOMEQLRQ 264

RESULT 5

AAR39481  
 ID AAR39481 standard; protein; 333 AA.

XX AAR39481;

XX 25-MAR-2003 (revised)  
 DT 28-JAN-1994 (first entry)

DE Human apoAIV mutein P(deltaC44) .

KW apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;  
 KW coronary disease; chylomicron; cholesterol transport; plaque deposition;  
 KW lecithin-cholesterol-acyltransferase; LCAT.

OS Synthetic.

Key Location/Qualifiers  
 Region 2..333  
 Region /label= P(deltaC44)  
 Region /note= "the 44 C-terminal amino acids of human apoAIV  
 have been deleted"

XX WO315198-A1.

XX 05-AUG-1993.

XX 26-JAN-1993; 93WO-FR000073.

XX 27-JAN-1992; 92FR-00000806.

XX (RHON ) RHONE POULENC RORER SA.

XX

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PI Denefle P, Guinet F, Latta M, Murry-Brellier A;
XX WPI; 1993-258676/32.
XX
XX New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug design
XX and/or treatment of hypercholesterolaemia.
XX
XX Claim 7; Page 31-32 and Page 4; 42pp; French.
XX
XX Human apolipoprotein AIV is a major component of chylomicrons in lymph
XX but is mainly found in the plasma in unassociated form. The apoAIV
XX mediates inverse transport of cholesterol. The invention covers
XX polypeptides which are derived from apoAIV by deletion of at least 10
XX terminal amino acids, by deletion of a helix or pair of helices, by
XX addition of a heterologous polypeptide portion or by a point mutation.
XX Such muteins are useful in the design of hypocholesterolaemic drugs to
XX treat hypercholesterolaemia and atherosclerosis. AAR39481 is a
XX specifically claimed mutein and the sequence has been compiled from the
XX wild-type sequence (see AAR39443) and the description given in the
XX disclosure; the mutant sequence is not shown in the specification.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 333 AA;
SQ
    Query Match          100.0%; Score 56; DB 2; Length 333;
    Best Local Similarity 100.0%; Pred. No. 0.22;
    Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KALVQQMQLRQ 12
DB 297 KALVQQMQLRQ 308
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|||||

RESULT 6
ID AAR39497 standard; protein; 333 AA.
XX
XX AAR39497;
XX
XX 25-MAR-2003 (revised)
XX 28-JAN-1994 (first entry)
XX
XX Human apoAIV mutein P(delta h5-6).
XX
XX apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;
XX coronary disease; chylomicron; cholesterol transport; plaque deposition;
XX lecithin-cholesterol-acyltransferase; LCAT.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Region 14..40
FT /note= "helix 1"
FT Region 41..62
FT /note= "helix 2"
FT Region 63..95
FT /note= "helix 3"
FT Region 96..117
FT /note= "helix 4"
FT Misc-difference 117..118
FT /note= "helices 5-6 have been deleted from between these
FT two sites"
FT
FT Region 118..139
FT /note= "helix 7"
FT Region 140..161
FT /note= "helix 8"
FT Region 162..183
FT /note= "helix 9"
FT Region 184..205
FT /note= "helix 10"
FT Region 206..223
FT /note= "helix 11"
FT Region 224..245
FT /note= "helix 12"
FT 246..267
FT /note= "helix 13"
FT 268..289
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FT 290..333
FT /note= "helix 15"
XX
XX WO9315198-A1.
XX
XX 05-AUG-1993.
XX
XX 26-JAN-1993; 93WO-FR0000073.
XX
XX 27-JAN-1992; 92FR-00000806.
XX
XX (RHON ) RHONE POULENC RORER SA.
XX
XX Denefle P, Guinet F, Latta M, Murry-Brellier A;
XX WPI; 1993-258676/32.
XX
XX New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug design
XX and/or treatment of hypercholesterolaemia.
XX
XX Claim 7; Page 31-32 and Page 5; 42pp; French.
XX
XX Human apolipoprotein AIV is a major component of chylomicrons in lymph
XX but is mainly found in the plasma in unassociated form. The apoAIV
XX mediates inverse transport of cholesterol. The invention covers
XX polypeptides which are derived from apoAIV by deletion of at least 10
XX terminal amino acids, by deletion of a helix or pair of helices, by
XX addition of a heterologous polypeptide portion or by a point mutation.
XX Such muteins are useful in the design of hypocholesterolaemic drugs to
XX treat hypercholesterolaemia and atherosclerosis. AAR39497 is a
XX specifically claimed mutein and the sequence has been compiled from the
XX wild-type sequence (see AAR39443) and the description given in the
XX disclosure; the mutant sequence is not shown in the specification.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 333 AA;
SQ
    Query Match          100.0%; Score 56; DB 2; Length 333;
    Best Local Similarity 100.0%; Pred. No. 0.22;
    Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KALVQQMQLRQ 12
DB 253 KALVQQMQLRQ 264
|||||
|||||

RESULT 7
ID AAR39490 standard; protein; 333 AA.
XX
XX AAR39490;
XX
XX 25-MAR-2003 (revised)
XX 28-JAN-1994 (first entry)
XX
XX Human apoAIV mutein P(delta h9-10).
XX
XX apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;
XX coronary disease; chylomicron; cholesterol transport; plaque deposition;
XX lecithin-cholesterol-acyltransferase; LCAT.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH Region 14..40
FT /note= "helix 1"
FT Region 41..62
FT /note= "helix 2"
FT 63..95
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 FT Region 162. .183  
 FT /note= "helix 7"  
 FT Region 184. .205  
 FT /note= "helix 8"  
 FT Misc-difference 205. .206  
 FT /note= "helices 9-10 have been deleted from between these  
 FT two sites"  
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 FT Region 224. .245  
 FT /note= "helix 12"  
 FT Region 246. .267  
 FT /note= "helix 13"  
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 FT /note= "helix 14"  
 FT Region 290. .333  
 FT /note= "helix 15"  
 XX  
 PN WO9315198-A1.  
 XX  
 XX 05-AUG-1993.  
 XX  
 XX 26-JAN-1993; 93WO-FR0000073.  
 XX  
 XX 27-JAN-1992; 92FR-00000806.  
 XX  
 XX (RHON ) RHONE POULENC RORER SA.  
 XX  
 XX Denefle P, Guinet F, Latta M, Murry-Brelrier A;  
 XX WPI; 1993-258676/32.  
 XX  
 XX New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug design  
 XX and/or treatment of hypercholesterolaemia.  
 XX  
 XX Claim 7; Page 31-32 and Page 5; 42pp; French.  
 XX  
 XX Human apolipoprotein AIV is a major component of chylomicrons in lymph  
 XX but is mainly found in the plasma in unassociated form. The apoAIV  
 XX mediates inverse transport of cholesterol. The invention covers  
 XX polypeptides which are derived from apoAIV by deletion of at least 10  
 XX terminal amino acids, by deletion of a helix or pair of helices, by  
 XX addition of a heterologous polypeptide portion or by a point mutation.  
 XX Such muteins are useful in the design of hypocholesterolaemic drugs to  
 XX treat hypercholesterolaemia and atherosclerosis. AAR39490 is a  
 XX specifically claimed mutein and the sequence has been compiled from the  
 XX wild-type sequence (see AAR39443) and the description given in the  
 XX disclosure; the mutant sequence is not shown in the specification.  
 XX (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 XX Sequence 333 AA;  
 XX  
 XX Query Match 100.0%; Score 56; DB 2; Length 333;  
 XX Best Local Similarity 100.0%; Pred. No. 0.22;  
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KALVQQMELRLQ 12  
 Db 253 KALVQQMELRLQ 264  
 RESULT 8  
 AAR39485  
 ID AAR39485 standard; protein; 337 AA.  
 XX

AC AAR39485;  
 XX  
 XX 25-MAR-2003 (revised)  
 XX 28-JAN-1994 (first entry)  
 XX  
 XX Human apoAIV mutein P(tag-delta h1-2).  
 DE  
 XX apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;  
 KW coronary disease; chylomicron; cholesterol transport; plaque deposition;  
 KW lecithin-cholesterol-acyltransferase; LCAT; tag purification marker.  
 XX  
 XX Synthetic.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FH Peptide 1. .10  
 FT /label= tag decapeptide  
 FT /note= "allows rapid, single stage purification without  
 FT affecting the properties of the mature mutein"  
 FT Misc-difference 22. .23  
 FT /note= "helices 1-2 have been deleted from between these  
 FT two sites"  
 FT Region 23. .55  
 FT /note= "helix 3"  
 FT Region 56. .77  
 FT /note= "helix 4"  
 FT Region 78. .99  
 FT /note= "helix 5"  
 FT Region 100. .121  
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 FT Region 122. .143  
 FT /note= "helix 7"  
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 FT /note= "helix 8"  
 FT Region 166. .187  
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 FT /note= "helix 10"  
 FT Region 210. .227  
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 FT Region 228. .249  
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 FT Region 272. .293  
 FT /note= "helix 14"  
 FT Region 294. .337  
 FT /note= "helix 15"  
 XX  
 XX WO9315198-A1.  
 PN  
 XX 05-AUG-1993.  
 XX  
 XX 26-JAN-1993; 93WO-FR0000073.  
 XX  
 XX 27-JAN-1992; 92FR-00000806.  
 XX  
 XX (RHON ) RHONE POULENC RORER SA.  
 XX  
 XX Denefle P, Guinet F, Latta M, Murry-Brelrier A;  
 XX WPI; 1993-258676/32.  
 XX  
 XX New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug design  
 XX and/or treatment of hypercholesterolaemia.  
 XX  
 XX Claim 7; Page 31-32 and Page 4; 42pp; French.  
 XX  
 XX Human apolipoprotein AIV is a major component of chylomicrons in lymph  
 XX but is mainly found in the plasma in unassociated form. The apoAIV  
 XX mediates inverse transport of cholesterol. The invention covers  
 XX polypeptides which are derived from apoAIV by deletion of at least 10  
 XX terminal amino acids, by deletion of a helix or pair of helices, by  
 XX addition of a heterologous polypeptide portion or by a point mutation.  
 XX Such muteins are useful in the design of hypocholesterolaemic drugs to  
 XX treat hypercholesterolaemia and atherosclerosis. AAR39490 is a  
 XX specifically claimed mutein and the sequence has been compiled from the  
 XX wild-type sequence (see AAR39443) and the description given in the  
 XX disclosure; the mutant sequence is not shown in the specification.  
 XX (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 XX Sequence 333 AA;  
 XX  
 XX Query Match 100.0%; Score 56; DB 2; Length 333;  
 XX Best Local Similarity 100.0%; Pred. No. 0.22;  
 XX Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KALVQQMELRLQ 12  
 Db 253 KALVQQMELRLQ 264  
 RESULT 8  
 AAR39485  
 ID AAR39485 standard; protein; 337 AA.  
 XX

CC Such muteins are useful in the design of hypocholesterolaemic drugs to  
 CC treat hypercholesterolaemia and atherosclerosis. AAR39485 is a  
 CC specifically claimed mutein and the sequence has been compiled from the  
 CC wild-type sequence (see AAR39443) and the description given in the  
 CC disclosure; the mutant sequence is not shown in the specification.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 XX SQ Sequence 337 AA;

Query Match 100.0%; Score 56; DB 2; Length 337;  
 Best Local Similarity 100.0%; Pred. No. 0.22; Indels 0; Gaps 0;  
 Matches 12; Conservative 0; Mismatches 0;

Qy 1 KALVQOMEQLRQ 12  
 |||||  
 Db 257 KALVQOMEQLRQ 268

RESULT 9  
 AAR39492  
 ID AAR39492 standard; protein; 337 AA.

XX AAR39492;

XX 25-MAR-2003 (revised)  
 DT 28-JAN-1994 (first entry)

XX Human apoAIV mutein P(delta h11-12).

XX apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;  
 KW coronary disease; chylomicron; cholesterol transport; plaque deposition;  
 KW lecithin-cholesterol-acyltransferase; LCAT.

XX Synthetic.

XX Key Location/Qualifiers  
 FH Region 14..40  
 FT /note= "helix 1"  
 FT Region 41..62  
 FT /note= "helix 2"  
 FT Region 63..95  
 FT /note= "helix 3"  
 FT Region 96..117  
 FT /note= "helix 4"  
 FT Region 118..139  
 FT /note= "helix 5"  
 FT Region 140..161  
 FT /note= "helix 6"  
 FT Region 162..183  
 FT /note= "helix 7"  
 FT Region 184..205  
 FT /note= "helix 8"  
 FT Region 206..227  
 FT /note= "helix 9"  
 FT Region 228..249  
 FT /note= "helix 10"  
 FT Misc-difference 249..250  
 FT /note= "helices 11-12 have been deleted from between  
 FT these two sites"  
 FT Region 250..271  
 FT /note= "helix 13"  
 FT Region 272..293  
 FT /note= "helix 14"  
 FT Region 294..337  
 FT /note= "helix 15"

XX WO9315198-A1.

XX 05-AUG-1993.

XX 26-JAN-1993; 93WO-FR0000073.

XX 27-JAN-1992; 92FR-00000806.

XX (RHON ) RHONE POULENC RORER SA.  
 XX PA  
 XX Denefle P, Guinet F, Latta M, Murry-Brelier A;  
 XX WPI; 1993-258676/32.  
 XX New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug design  
 XX and/or treatment of hypercholesterolaemia.

XX Claim 7; Page 31-32 and Page 5; 42pp; French.

XX Human apolipoprotein AIV is a major component of chylomicrons in lymph  
 CC but is mainly found in the plasma in unassociated form. The apoAIV  
 CC mediates inverse transport of cholesterol. The invention covers  
 CC polypeptides which are derived from apoAIV by deletion of at least 10  
 CC terminal amino acids, by deletion of a helix or pair of helices, by  
 CC addition of a heterologous polypeptide portion or by a point mutation.  
 CC Such muteins are useful in the design of hypocholesterolaemic drugs to  
 CC treat hypercholesterolaemia and atherosclerosis. AAR39492 is a  
 CC specifically claimed mutein and the sequence has been compiled from the  
 CC wild-type sequence (see AAR39443) and the description given in the  
 CC disclosure; the mutant sequence is not shown in the specification.  
 CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 337 AA;

Query Match 100.0%; Score 56; DB 2; Length 337;

Best Local Similarity 100.0%; Pred. No. 0.22; Indels 0; Gaps 0;  
 Matches 12; Conservative 0; Mismatches 0;

Qy 1 KALVQOMEQLRQ 12  
 |||||  
 Db 257 KALVQOMEQLRQ 268

RESULT 10

AAR39494

ID AAR39494 standard; protein; 337 AA.

XX AAR39494;

XX 25-MAR-2003 (revised)

DT 28-JAN-1994 (first entry)

XX Human apoAIV mutein P(delta h11-12, L87M).

XX apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;  
 KW coronary disease; chylomicron; cholesterol transport; plaque deposition;  
 KW lecithin-cholesterol-acyltransferase; LCAT.

XX Synthetic.

XX Key Location/Qualifiers  
 FH Protein 2..337  
 FT /label= (delta h11-12, L87M)  
 FT /note= "helices 11-12 have been deleted from mature human  
 FT apoAIV and wild-type Leu87 has been substd. by Met"  
 FT Region 14..40  
 FT /note= "helix 1"  
 FT Region 41..62  
 FT /note= "helix 2"  
 FT Region 63..95  
 FT /note= "helix 3"  
 FT Misc-difference 87  
 FT /note= "L87M"  
 FT Region 96..117  
 FT /note= "helix 4"  
 FT Region 118..139  
 FT /note= "helix 5"  
 FT Region 140..161  
 FT /note= "helix 6"  
 FT Region 162..183







PT and/or treatment of hypercholesterolaemia.  
 XX Claim 7; Page 31-32 and Page 4; 42pp; French.  
 XX Human apolipoprotein AIV is a major component of chylomicrons in lymph  
 CC but is mainly found in the plasma in unassociated form. The apoAIV  
 CC mediates inverse transport of cholesterol. The invention covers  
 CC polypeptides which are derived from apoAIV by deletion of at least 10  
 CC terminal amino acids, by deletion of a helix or pair of helices, by  
 CC addition of a heterologous polypeptide portion or by a point mutation.  
 CC Such muteins are useful in the design of hypocholesterolaemic drugs to  
 CC treat hypercholesterolaemia and atherosclerosis. AAR39489 is a  
 CC specifically claimed mutein and the sequence has been compiled from the  
 CC wild-type sequence (see AAR39443) and the description given in the  
 CC disclosure; the mutant sequence is not shown in the specification.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX Sequence 342 AA;  
 SQ

Query Match 100.0%; Score 56; DB 2; Length 342;  
 Best Local Similarity 100.0%; Pred. No. 0.23;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KALVQOMEQLRQ 12  
 DB 262 KALVQOMEQLRQ 273

RESULT 14  
 AAR39498  
 ID AAR39498 standard; protein; 342 AA.  
 AC AAR39498;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 28-JAN-1994 (first entry)  
 XX  
 XX Human apoAIV mutein P (tag-delta h5-6).  
 XX apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;  
 KW coronary disease; chylomicron; cholesterol transport; plaque deposition;  
 KW lecithin-cholesterol-acyltransferase; LCAT; tag purification marker.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 FT Peptide 1..10  
 FT /label= tag\_decapeptide  
 FT /note= "allows rapid, single stage purification without  
 FT affecting the properties of the mature mutein"  
 FT 23..49  
 FT /note= "helix 1"  
 FT Region 50..71  
 FT /note= "helix 2"  
 FT Region 72..104  
 FT /note= "helix 3"  
 FT Region 105..126  
 FT /note= "helix 4"  
 FT Misc-difference 126..127  
 FT /note= "helices 5-6 have been deleted from between these  
 FT two sites"  
 FT Region 127..148  
 FT /note= "helix 7"  
 FT Region 149..170  
 FT /note= "helix 8"  
 FT Region 171..192  
 FT /note= "helix 9"  
 FT Region 193..214  
 FT /note= "helix 10"  
 FT Region 215..232  
 FT /note= "helix 11"  
 FT Region 233..254  
 FT /note= "helix 12"

FT Region 255..276  
 FT /note= "helix 13"  
 FT Region 277..298  
 FT /note= "helix 14"  
 FT Region 299..342  
 FT /note= "helix 15"  
 XX  
 PN WO9315198-A1.  
 XX 05-AUG-1993.  
 XX 26-JAN-1993; 93WO-PR0000073.  
 XX 27-JAN-1992; 92FR-00000806.  
 XX (RHON ) RHONE POULENC RORER SA.  
 PA  
 PI Denefle P, Guinet F, Latta M, Murry-Brellier A;  
 XX WPI; 1993-258676/32.  
 DR  
 XX New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug design  
 PT and/or treatment of hypercholesterolaemia.  
 PT  
 XX Claim 7; Page 31-32 and Page 5; 42pp; French.  
 PS  
 XX Human apolipoprotein AIV is a major component of chylomicrons in lymph  
 CC but is mainly found in the plasma in unassociated form. The apoAIV  
 CC mediates inverse transport of cholesterol. The invention covers  
 CC polypeptides which are derived from apoAIV by deletion of at least 10  
 CC terminal amino acids, by deletion of a helix or pair of helices, by  
 CC addition of a heterologous polypeptide portion or by a point mutation.  
 CC Such muteins are useful in the design of hypocholesterolaemic drugs to  
 CC treat hypercholesterolaemia and atherosclerosis. AAR39498 is a  
 CC specifically claimed mutein and the sequence has been compiled from the  
 CC wild-type sequence (see AAR39443) and the description given in the  
 CC disclosure; the mutant sequence is not shown in the specification.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX Sequence 342 AA;  
 SQ

Query Match 100.0%; Score 56; DB 2; Length 342;  
 Best Local Similarity 100.0%; Pred. No. 0.23;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KALVQOMEQLRQ 12  
 DB 262 KALVQOMEQLRQ 273

RESULT 15  
 AAR39493  
 ID AAR39493 standard; protein; 346 AA.  
 AC AAR39493;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 28-JAN-1994 (first entry)  
 XX  
 XX Human apoAIV mutein P (tag-delta h11-12).  
 DE apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;  
 KW coronary disease; chylomicron; cholesterol transport; plaque deposition;  
 KW lecithin-cholesterol-acyltransferase; LCAT; tag purification marker.  
 XX Synthetic.  
 XX Key Location/Qualifiers  
 FT Peptide 1..10  
 FT /label= tag\_decapeptide  
 FT /note= "allows rapid, single stage purification without  
 FT affecting the properties of the mature mutein"  
 FT 23..49  
 FT /note= "helix 12"

FT Region /note= "helix 1"  
 FT 50. .71  
 FT /note= "helix 2"  
 FT 72. .104  
 FT /note= "helix 3"  
 FT 105. .126  
 FT /note= "helix 4"  
 FT 127. .148  
 FT /note= "helix 5"  
 FT 149. .170  
 FT /note= "helix 6"  
 FT 171. .192  
 FT /note= "helix 7"  
 FT 193. .214  
 FT /note= "helix 8"  
 FT 215. .236  
 FT /note= "helix 9"  
 FT 237. .258  
 FT /note= "helix 10"  
 FT 258. .259  
 FT /note= "helices 11-12 have been deleted from between  
 FT these two sites"  
 FT 259. .280  
 FT /note= "helix 13"  
 FT 281. .302  
 FT /note= "helix 14"  
 FT 303. .346  
 FT /note= "helix 15"  
 FT  
 XX WO9315198-A1.  
 XX  
 XX 05-AUG-1993.  
 XX  
 XX 26-JAN-1993; 93WO-FR0000073.  
 XX  
 XX 27-JAN-1992; 92FR-00000806.  
 XX  
 XX (RHON ) RHONE POULENC RORER SA.  
 XX  
 XX Denefle P, Guinet F, Latta M, Murry-Brellier A;  
 XX WPI; 1993-258676/32.  
 XX  
 XX New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug design  
 XX and/or treatment of hypercholesterolaemia.  
 XX  
 XX Claim 7; Page 31-32 and Page 5; 42pp; French.  
 XX  
 XX Human apolipoprotein AIV is a major component of chylomicrons in lymph  
 XX but is mainly found in the plasma in unassociated form. The apoAIV  
 XX mediates inverse transport of cholesterol. The invention covers  
 XX polypeptides which are derived from apoAIV by deletion of at least 10  
 XX terminal amino acids, by deletion of a helix or pair of helices, by  
 XX addition of a heterologous polypeptide portion or by a point mutation.  
 XX Such muteins are useful in the design of hypocholesterolaemic drugs to  
 XX treat hypercholesterolaemia and atherosclerosis. AAR39493 is a  
 XX specifically claimed mutein and the sequence has been compiled from the  
 XX wild-type sequence (see AAR39443) and the description given in the  
 XX disclosure; the mutant sequence is not shown in the specification.  
 XX (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 XX Sequence 346 AA;  
 SQ  
 Query Match 100.0%; Score 56; DB 2; Length 346;  
 Best Local Similarity 100.0%; Pred. NO. 0.23;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KALVQOMEQLRQ 12  
 DB 266 KALVQOMEQLRQ 277  
 RESULT 16

AAR39478  
 ID AAR39478 standard; protein; 363 AA.  
 XX  
 AC AAR39478;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 28-JAN-1994 (first entry)  
 XX  
 DE Human apoAIV mutein P(deltan13, R93G).  
 XX  
 KW apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;  
 KW coronary disease; chylomicron; cholesterol transport; plaque deposition;  
 KW lecithin-cholesterol-acyltransferase; LCAT.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Protein 1..363  
 FT /label= (deltan13, R93G)  
 FT /note= "the 13 N-terminal amino acids of human apoAIV  
 FT have been deleted and wild-type Arg93 has been substd. by  
 FT Gly"  
 FT Misc-difference 79  
 FT /note= "R93G"  
 FT  
 FT WO9315198-A1.  
 PN  
 PD 05-AUG-1993.  
 XX  
 XX 26-JAN-1993; 93WO-FR0000073.  
 XX  
 XX 27-JAN-1992; 92FR-00000806.  
 XX  
 XX (RHON ) RHONE POULENC RORER SA.  
 XX  
 XX Denefle P, Guinet F, Latta M, Murry-Brellier A;  
 XX WPI; 1993-258676/32.  
 XX  
 XX New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug design  
 XX and/or treatment of hypercholesterolaemia.  
 XX  
 XX Claim 7; Page 31-32 and Page 4; 42pp; French.  
 XX  
 XX Human apolipoprotein AIV is a major component of chylomicrons in lymph  
 XX but is mainly found in the plasma in unassociated form. The apoAIV  
 XX mediates inverse transport of cholesterol. The invention covers  
 XX polypeptides which are derived from apoAIV by deletion of at least 10  
 XX terminal amino acids, by deletion of a helix or pair of helices, by  
 XX addition of a heterologous polypeptide portion or by a point mutation.  
 XX Such muteins are useful in the design of hypocholesterolaemic drugs to  
 XX treat hypercholesterolaemia and atherosclerosis. AAR39478 is a  
 XX specifically claimed mutein and the sequence has been compiled from the  
 XX wild-type sequence (see AAR39443) and the description given in the  
 XX disclosure; the mutant sequence is not shown in the specification.  
 XX (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 XX Sequence 363 AA;  
 SQ  
 Query Match 100.0%; Score 56; DB 2; Length 363;  
 Best Local Similarity 100.0%; Pred. NO. 0.24;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 KALVQOMEQLRQ 12  
 DB 283 KALVQOMEQLRQ 294  
 RESULT 17  
 AAR39479  
 ID AAR39479 standard; protein; 363 AA.  
 XX  
 AC AAR39479;

XX 25-MAR-2003 (revised)  
 DT 28-JAN-1994 (first entry)  
 XX Human apoAIV mutein P(deltaN13).  
 DE  
 XX  
 XX apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;  
 KW coronary disease; chylomicron; cholesterol transport; plaque deposition;  
 KW lecithin-cholesterol-acyltransferase; LCAT.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH 1..363  
 FT Protein /label= P(deltaN13)  
 FT /note= "the 13 N-terminal amino acids of mature human  
 FT apoAIV have been deleted"  
 XX  
 XX WO9315198-A1.  
 PN  
 XX 05-AUG-1993.  
 PD  
 XX 26-JAN-1993; 93WO-FR0000073.  
 PP  
 XX 27-JAN-1992; 92FR-00000806.  
 PR  
 XX (RHON ) RHONE POULENC RORER SA.  
 PA  
 XX Denefle P, Guinet F, Latta M, Murry-Brelier A;  
 PI WPI; 1993-258676/32.  
 DR  
 XX New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug design  
 XX and/or treatment of hypercholesterolaemia.  
 XX  
 XX Claim 7; Page 31-32 and Page 4; 42pp; French.  
 XX  
 XX Human apolipoprotein AIV is a major component of chylomicrons in lymph  
 CC but is mainly found in the plasma in unassociated form. The apoAIV  
 CC mediates inverse transport of cholesterol. The invention covers  
 CC polypeptides which are derived from apoAIV by deletion of at least 10  
 CC terminal amino acids, by deletion of a helix or pair of helices, by  
 CC addition of a heterologous polypeptide portion or by a point mutation.  
 CC Such muteins are useful in the design of hypocholesterolaemic drugs to  
 CC treat hypercholesterolaemia and atherosclerosis. AAR39479 is a  
 CC specifically claimed mutein and the sequence has been compiled from the  
 CC wild-type sequence (see AAR39443) and the description given in the  
 CC disclosure; the mutant sequence is not shown in the specification.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 363 AA;  
 Query Match 100.0%; Score 56; DB 2; Length 363;  
 Best Local Similarity 100.0%; Pred. No. 0.24;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KALVQOMEQLRQ 12  
 |||||  
 Db 283 KALVQOMEQLRQ 294  
 |||||  
 RESULT 18  
 AAR39486  
 ID AAR39486 standard; protein; 373 AA.  
 XX  
 AC AAR39486;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 28-JAN-1994 (first entry)  
 XX  
 DE Human apoAIV mutein P(tag-deltaN13).  
 XX  
 KW apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;

KW coronary disease; chylomicron; cholesterol transport; plaque deposition;  
 KW lecithin-cholesterol-acyltransferase; LCAT; tag purification marker.  
 XX  
 OS Synthetic.  
 XX  
 XX Key Location/Qualifiers  
 FH 1..110  
 FT Peptide /label= tag-decapeptide  
 FT /note= "allows rapid, single stage purification without  
 FT affecting the properties of the mature mutein"  
 FT 11..373  
 FT Protein /label= P(deltaN13)  
 FT /note= "the 13 N-terminal amino acids of mature human  
 FT apoAIV have been deleted"  
 XX  
 XX WO9315198-A1.  
 PN  
 XX 05-AUG-1993.  
 PD  
 XX 26-JAN-1993; 93WO-FR0000073.  
 PP  
 XX 27-JAN-1992; 92FR-00000806.  
 PR  
 XX (RHON ) RHONE POULENC RORER SA.  
 PA  
 XX Denefle P, Guinet F, Latta M, Murry-Brelier A;  
 PI WPI; 1993-258676/32.  
 DR  
 XX New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug design  
 XX and/or treatment of hypercholesterolaemia.  
 XX  
 XX Claim 7; Page 31-32 and Page 4; 42pp; French.  
 XX  
 XX Human apolipoprotein AIV is a major component of chylomicrons in lymph  
 CC but is mainly found in the plasma in unassociated form. The apoAIV  
 CC mediates inverse transport of cholesterol. The invention covers  
 CC polypeptides which are derived from apoAIV by deletion of at least 10  
 CC terminal amino acids, by deletion of a helix or pair of helices, by  
 CC addition of a heterologous polypeptide portion or by a point mutation.  
 CC Such muteins are useful in the design of hypocholesterolaemic drugs to  
 CC treat hypercholesterolaemia and atherosclerosis. AAR39486 is a  
 CC specifically claimed mutein and the sequence has been compiled from the  
 CC wild-type sequence (see AAR39443) and the description given in the  
 CC disclosure; the mutant sequence is not shown in the specification.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 373 AA;  
 Query Match 100.0%; Score 56; DB 2; Length 373;  
 Best Local Similarity 100.0%; Pred. No. 0.25;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 KALVQOMEQLRQ 12  
 |||||  
 Db 293 KALVQOMEQLRQ 304  
 |||||  
 RESULT 19  
 AAR39502  
 ID AAR39502 standard; protein; 377 AA.  
 XX  
 AC AAR39502;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 28-JAN-1994 (first entry)  
 XX  
 DE Human apoAIV mutein P(D5K).  
 XX  
 KW apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;  
 KW coronary disease; chylomicron; cholesterol transport; plaque deposition;  
 KW lecithin-cholesterol-acyltransferase; LCAT.  
 XX

OS Synthetic.

XX Key Location/Qualifiers

PH Protein 2..377

FT /note= "mature P(D5K)"

FT Misc-difference 6

FT /note= "wild-type Asp5 is substd. by Lys"

FT Region 14..40

FT /note= "helix 1"

FT Region 41..62

FT /note= "helix 2"

FT Region 63..95

FT /note= "helix 3"

FT Region 96..117

FT /note= "helix 4"

FT Region 118..139

FT /note= "helix 5"

FT Region 140..161

FT /note= "helix 6"

FT Region 162..183

FT /note= "helix 7"

FT Region 184..205

FT /note= "helix 8"

FT Region 206..227

FT /note= "helix 9"

FT Region 228..249

FT /note= "helix 10"

FT Region 250..267

FT /note= "helix 11"

FT Region 268..289

FT /note= "helix 12"

FT Region 290..311

FT /note= "helix 13"

FT Region 312..333

FT /note= "helix 14"

FT Region 334..377

FT /note= "helix 15"

XX WO9315198-A1.

PN 05-AUG-1993.

XX 26-JAN-1993; 93WO-FR0000073.

XX 27-JAN-1992; 92FR-00000806.

PR (RHON ) RHONE POULENC RORER SA.

PA Denefle P, Guinet F, Latta M, Murry-Brelrier A;

PI WPI; 1993-258676/32.

XX New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug design

PT and/or treatment of hypercholesterolaemia.

XX Claim 7; Page 31-32 and Page 5; 42pp; French.

CC Human apolipoprotein AIV is a major component of chylomicrons in lymph

CC but is mainly found in the plasma in unassociated form. The apo AIV

CC mediates inverse transport of cholesterol. The invention covers

CC polypeptides which are derived from apoAIV by deletion of at least 10

CC terminal amino acids, by deletion of a helix or pair of helices, by

CC addition of a heterologous polypeptide portion or by a point mutation.

CC Such mutants are useful in the design of hypocholesterolaemic drugs to

CC treat hypercholesterolaemia and atherosclerosis. AAR39502 is a

CC specifically claimed nucleic acid and the sequence has been compiled from the

CC wild-type sequence (see AAR39443) and the description given in the

CC disclosure; the mutant sequence is not shown in the specification.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 377 AA;

SQ Query Match 100.0%; Score 56; DB 2; Length 377;

Best Local Similarity 100.0%; Pred. No. 0.25;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KALVQOMEQLRQ 12

DB 297 KALVQOMEQLRQ 308

RESULT 20

AAR39443

ID AAR39443 standard; protein; 377 AA.

XX AAR39443;

XX 25-MAR-2003 (revised)

DT 28-JAN-1994 (first entry)

XX Human apolipoprotein AIV.

XX apolipoprotein AIV; apoAIV; hypercholesterolaemia; atherosclerosis;

KW coronary disease; chylomicron; cholesterol transport; plaque deposition;

KW lecithin-cholesterol-acyltransferase; LCAT.

XX Homo sapiens.

XX Key Location/Qualifiers

FT Region 14..40

FT /note= "helix 1"

FT Region 41..62

FT /note= "helix 2"

FT Region 63..95

FT /note= "helix 3"

FT Region 96..117

FT /note= "helix 4"

FT Region 118..139

FT /note= "helix 5"

FT Region 140..161

FT /note= "helix 6"

FT Region 162..183

FT /note= "helix 7"

FT Region 184..205

FT /note= "helix 8"

FT Region 206..227

FT /note= "helix 9"

FT Region 228..249

FT /note= "helix 10"

FT Region 250..267

FT /note= "helix 11"

FT Region 268..289

FT /note= "helix 12"

FT Region 290..311

FT /note= "helix 13"

FT Region 312..333

FT /note= "helix 14"

FT Region 334..377

FT /note= "helix 15"

XX WO9315198-A1.

PN 05-AUG-1993.

XX 26-JAN-1993; 93WO-FR0000073.

XX 27-JAN-1992; 92FR-00000806.

PR (RHON ) RHONE POULENC RORER SA.

PA Denefle P, Guinet F, Latta M, Murry-Brelrier A;

PI WPI; 1993-258676/32.

DR N-PSDB; AAQ43306.

XX New apo:lipoprotein AIV mutant polypeptide(s) - useful for drug design

PT and/or treatment of hypercholesterolaemia.

XX  
PS Disclosure; Page 32-33; 42pp; French.  
XX  
CC Human apolipoprotein AIV is a major component of chylomicrons in lymph  
CC but is mainly found in the plasma in unassociated form. The apo AIV  
CC mediates inverse transport of cholesterol. The invention covers  
CC polypeptides which are derived from apoAIV by deletion of at least 10  
CC terminal amino acids, by deletion of a helix or pair of helices, by  
CC addition of a heterologous polypeptide portion or by a point mutation.  
CC Such mutants are useful in the design of hypocholesterolaemic drugs to  
CC treat hypercholesterolaemia and atherosclerosis. (Updated on 25-MAR-2003  
XX to correct PN field.)

SQ Sequence 377 AA;

Query Match 100.0%; Score 56; DB 2; Length 377;  
Best Local Similarity 100.0%; Pred. No. 0.25;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KALVQOMEQLRQ 12  
| | | | | | | | | |  
Db 297 KALVQOMEQLRQ 308

Search completed: April 14, 2006, 13:09:22  
Job time : 191 secs

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OM protein - protein search, using sw model

Run on: April 14, 2006, 13:13:49 ; Search time 48 Seconds  
(without alignments)  
20.669 Million cell updates/sec

Title: US-09-991-809-1  
Perfect score: 56  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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5: /cgn2\_6/ptodata/1/iaa/RE COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	396	2	US-09-800-729-207
2	56	100.0	396	2	US-09-987-107-33
3	56	100.0	397	2	US-09-079-030-123
4	56	100.0	401	2	US-09-987-107-36
5	56	100.0	426	2	US-09-949-016-10854
6	56	100.0	429	2	US-09-987-107-34
7	51	91.1	28	1	US-08-408-858A-10
8	49	87.5	391	2	US-09-800-729-208
9	49	87.5	395	2	US-09-987-107-35
10	47	83.9	382	2	US-09-800-729-206
11	47	83.9	382	2	US-09-987-107-37
12	43	76.8	30	1	US-08-408-858A-7
13	43	76.8	391	2	US-09-987-107-38
14	38	67.9	498	2	US-10-104-047-3191
15	38	67.9	500	2	US-09-252-991A-30255
16	37	66.1	107	2	US-09-668-119-6
17	37	66.1	579	2	US-09-668-119-3
18	36	64.3	115	2	US-09-513-999C-4946
19	36	64.3	138	2	US-09-513-999C-4945
20	36	64.3	434	2	US-09-328-352-4261
21	35	62.5	195	2	US-09-489-039A-7190
22	35	62.5	732	2	US-08-671-757A-7
23	35	62.5	732	2	US-08-671-757A-8
24	35	62.5	732	2	US-09-015-078-7
25	35	62.5	732	2	US-09-015-078-8
26	35	62.5	732	2	US-10-238-977A-7
27	35	62.5	732	2	US-10-238-977A-8

28	35	62.5	915	2	US-09-949-016-7425	Sequence 7425, Ap
29	35	62.5	956	2	US-09-914-259-17	Sequence 17, Appl
30	35	62.5	957	2	US-09-914-259-16	Sequence 16, Appl
31	35	62.5	1938	2	US-09-949-016-6417	Sequence 6417, Ap
32	35	62.5	1939	2	US-09-949-016-8134	Sequence 8134, Ap
33	35	62.5	2568	2	US-09-866-108A-3	Sequence 3, Appli
34	35	62.5	3854	2	US-09-949-016-7876	Sequence 7876, Ap
35	35	62.5	5024	2	US-09-710-279-2964	Sequence 2964, Ap
36	35	62.5	10182	2	US-09-134-001C-3159	Sequence 3159, Ap
37	34	60.7	142	2	US-09-543-681A-5092	Sequence 5092, Ap
38	34	60.7	155	2	US-09-270-767-35116	Sequence 35116, A
39	34	60.7	155	2	US-09-270-767-35116	Sequence 50333, A
40	34	60.7	368	2	US-09-533-029-8	Sequence 8, Appli
41	34	60.7	724	2	US-09-328-352-7710	Sequence 7710, Ap
42	34	60.7	816	2	US-09-543-681A-7118	Sequence 7118, Ap
43	34	60.7	1085	1	US-08-431-080-28	Sequence 28, Appl
44	34	60.7	1085	1	US-08-938-534-28	Sequence 28, Appl
45	34	60.7	1085	2	US-09-345-294-28	Sequence 28, Appl

## ALIGNMENTS

### RESULT 1

US-09-800-729-207  
; Sequence 207, Application US/09800729  
; Patent No. 6605592  
; GENERAL INFORMATION:  
; APPLICANT: Ni et al.  
; TITLE OF INVENTION: 32 Human secreted proteins  
; FILE REFERENCE: P2044P1  
; CURRENT APPLICATION NUMBER: US/09/800.729  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: PCT/US00/26013  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: 60/155,709  
; PRIOR FILING DATE: 1999-09-24  
; NUMBER OF SEQ ID NOS: 217  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 207  
; TYPE: PRT  
; LENGTH: 396  
; ORGANISM: Homo sapiens  
US-09-800-729-207

Query Match 100.0% Score 56; DB 2; Length 396;  
Best Local Similarity 100.0%; Pred. No. 0.064;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12  
Db 316 KALVQOMEQLRQ 327

### RESULT 2

US-09-987-107-33  
; Sequence 33, Application US/09987107  
; Patent No. 6897039  
; GENERAL INFORMATION:  
; APPLICANT: GRAVERSEN, Jonas  
; APPLICANT: MOESTRUP, Soren  
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES  
; FILE REFERENCE: GRAVERSENIA  
; CURRENT APPLICATION NUMBER: US/09/987.107  
; CURRENT FILING DATE: 2001-11-13  
; PRIOR APPLICATION NUMBER: US 60/264,022  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: DK PA2001 00057  
; PRIOR FILING DATE: 2001-01-15  
; PRIOR APPLICATION NUMBER: DK PA2000 01682  
; PRIOR FILING DATE: 2000-11-10  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 33
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-987-107-33

Query Match          100.0%; Score 56; DB 2; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12
Db 316 KALVQOMEQLRQ 327

RESULT 3
US-09-079-030-123
; Sequence 123, Application US/09079030
; Patent No. 6635623
; GENERAL INFORMATION:
; APPLICANT: Guevera, Jr., Juan G.
; APPLICANT: Hoogeveen, Ron C.
; APPLICANT: Moore, Paul J.
; TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY
; TITLE OF INVENTION: VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS
; NUMBER OF SEQUENCES: 229
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,030
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMillian, Nabeela R.
; REGISTRATION NUMBER: P-43,363
; REFERENCE/DOCKET NUMBER: ARAG:003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-079-030-123

Query Match          100.0%; Score 56; DB 2; Length 397;
Best Local Similarity 100.0%; Pred. No. 0.064;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12
Db 317 KALVQOMEQLRQ 328

RESULT 4
US-09-987-107-36
; Sequence 36, Application US/09987107
; Patent No. 6897039
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
```

```
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 36
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Papio anubis
US-09-987-107-36

Query Match          100.0%; Score 56; DB 2; Length 401;
Best Local Similarity 100.0%; Pred. No. 0.065;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12
Db 300 KALVQOMEQLRQ 311

RESULT 5
US-09-949-016-10854
; Sequence 10854, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Pstseq for Windows Version 4.0
; SEQ ID NO 10854
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-10854

Query Match          100.0%; Score 56; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12
Db 346 KALVQOMEQLRQ 357

RESULT 6
US-09-987-107-34
; Sequence 34, Application US/09987107
; Patent No. 6897039
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
```



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; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-09-987-107-34

Query Match      100.0%; Score 56; DB 2; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.069;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 KALVQOMEQLRQ 12
      |||||:|||||
Db      316 KALVQOMEQLRQ 327

RESULT 7
US-08-408-858A-10
; Sequence 10, Application US/08408858A
; Patent No. 5840688
; GENERAL INFORMATION:
; APPLICANT: Tso, Patrick
; TITLE OF INVENTION: EATING SUPPRESSANT PEPTIDES
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,858A
; FILING DATE: 22-MAR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 90212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-408-858A-10

Query Match      91.1%; Score 51; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.03;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 ALVQOMEQLRQ 12
      |||||:|||||
Db      1 ALVQOMEQLRQ 11

RESULT 8

```

```

US-09-800-729-208
; Sequence 208, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: PZ044P1
; CURRENT APPLICATION NUMBER: US/09/800,729
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 208
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-208

Query Match      87.5%; Score 49; DB 2; Length 391;
Best Local Similarity 83.3%; Pred. No. 0.97;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KALVQOMEQLRQ 12
      |||||:|||||
Db      316 KALVQOMEQLRQ 327

RESULT 9
US-09-987-107-35
; Sequence 35, Application US/09987107
; Patent No. 6897039
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-987-107-35

Query Match      87.5%; Score 49; DB 2; Length 395;
Best Local Similarity 83.3%; Pred. No. 0.98;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KALVQOMEQLRQ 12
      |||||:|||||
Db      316 KALVQOMEQLRQ 327

RESULT 10
US-09-800-729-206
; Sequence 206, Application US/09800729
; Patent No. 6605592
; GENERAL INFORMATION:
; APPLICANT: Ni et al.
; TITLE OF INVENTION: 32 Human secreted proteins
; FILE REFERENCE: PZ044P1
; CURRENT APPLICATION NUMBER: US/09/800,729

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; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: PCT/US00/26013
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 60/155,709
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 217
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 206
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-800-729-206

Query Match      83.9%; Score 47; DB 2; Length 382;
Best Local Similarity 83.3%; Pred. No. 2.1;
Matches 10; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 KALVQMEQLRQ 12
|||||: |||
Db 316 KALVQVVEDLRQ 327

RESULT 11
US-09-987-107-37
; Sequence 37, Application US/09987107
; Patent No. 6897039
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Sus scrofa
US-09-987-107-37

Query Match      83.9%; Score 47; DB 2; Length 382;
Best Local Similarity 83.3%; Pred. No. 2.1;
Matches 10; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 1 KALVQMEQLRQ 12
|||||: |||
Db 316 KALVQVVEDLRQ 327

RESULT 12
US-08-408-858A-7
; Sequence 7, Application US/08408858A
; Patent No. 5840688
; GENERAL INFORMATION:
; APPLICANT: Tso, Patrick
; TITLE OF INVENTION: EATING SUPPRESSANT PEPTIDES
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: USA
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/408,858A
; APPLICATION NUMBER: US/08/408,858A
; FILING DATE: 22-MAR-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 90212
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516-742-4343
; TELEFAX: 516-742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 30 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-408-858A-7

Query Match      76.8%; Score 43; DB 1; Length 30;
Best Local Similarity 81.8%; Pred. No. 0.74;
Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 2 ALVQOMEQLRQ 12
|||||: |||
Db 1 ALVQOMEKFRQ 11

RESULT 13
US-09-987-107-38
; Sequence 38, Application US/09987107
; Patent No. 6897039
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-987-107-38

Query Match      76.8%; Score 43; DB 2; Length 391;
Best Local Similarity 81.8%; Pred. No. 10;
Matches 9; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

Qy 2 ALVQOMEQLRQ 12
|||||: |||
Db 317 ALVQOMEKFRQ 327

RESULT 14
US-10-104-047-3191
; Sequence 3191, Application US/10104047
; Patent No. 6943241
; GENERAL INFORMATION:
; APPLICANT: HELIX RESEARCH INSTITUTE
```

; TITLE OF INVENTION: No. 6943241el full length cDNA  
; FILE REFERENCE: H1-A0105  
; CURRENT APPLICATION NUMBER: US/10/104,047  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER:  
; PRIOR FILING DATE:  
; NUMBER OF SEQ ID NOS: 4096  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3191  
; LENGTH: 498  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-104-047-3191

Query Match 67.9%; Score 38; DB 2; Length 498;  
Best Local Similarity 63.6%; Pred. No. 92;  
Matches 7; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLR 11  
:|:|:|:|:|:  
Db 218 BALVQOMEELK 228

RESULT 15  
US-09-252-991A-30255  
; Sequence 30255, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
; FILE REFERENCE: 107196.136  
; CURRENT APPLICATION NUMBER: US/09/252.991A  
; CURRENT FILING DATE: 1999-02-18  
; PRIOR APPLICATION NUMBER: US 60/074,788  
; PRIOR FILING DATE: 1998-02-18  
; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 30255  
; LENGTH: 500  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-30255

Query Match 67.9%; Score 38; DB 2; Length 500;  
Best Local Similarity 80.0%; Pred. No. 92;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 LVQOMEQLRQ 12  
:|:|:|:|:|:  
Db 365 LLQQAELRQ 374

RESULT 16  
US-09-668-119-6  
; Sequence 6, Application US/09668119  
; Patent No. 6768003  
; GENERAL INFORMATION:  
; APPLICANT: Solomon, William B  
; APPLICANT: Abraham, Shaji  
; TITLE OF INVENTION: Transcriptional adaptor protein  
; FILE REFERENCE: 011.00250  
; CURRENT APPLICATION NUMBER: US/09/668,119  
; CURRENT FILING DATE: 2000-09-22  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 107  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-668-119-6

Query Match 66.1%; Score 37; DB 2; Length 107;  
Best Local Similarity 58.3%; Pred. No. 28;  
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12  
:|:|:|:|:|:  
Db 43 QAVVQQQQQLQQ 54

RESULT 17  
US-09-668-119-3  
; Sequence 3, Application US/09668119  
; Patent No. 6768003  
; GENERAL INFORMATION:  
; APPLICANT: Solomon, William B  
; APPLICANT: Abraham, Shaji  
; TITLE OF INVENTION: Transcriptional adaptor protein  
; FILE REFERENCE: 011.00250  
; CURRENT APPLICATION NUMBER: US/09/668,119  
; CURRENT FILING DATE: 2000-09-22  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 579  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-668-119-3

Query Match 66.1%; Score 37; DB 2; Length 579;  
Best Local Similarity 58.3%; Pred. No. 1.6e+02;  
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12  
:|:|:|:|:|:  
Db 175 QAVVQQQQQLQQ 186

RESULT 18  
US-09-513-999C-4946  
; Sequence 4946, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; FILE REFERENCE: 59.US2.REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 4946  
; LENGTH: 115  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 115  
; OTHER INFORMATION: Xaa=His or Gln  
US-09-513-999C-4946

Query Match 64.3%; Score 36; DB 2; Length 115;  
Best Local Similarity 63.6%; Pred. No. 45;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLR 11  
|:|:|:|:|:  
Db 8 KGLVRQLEQFR 18

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RESULT 19
US-09-513-999C-4945
; Sequence 4945, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513.999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 4945
; LENGTH: 138
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-4945

Query Match      64.3%; Score 36; DB 2; Length 138;
Best Local Similarity 63.6%; Pred. No. 54;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLR 11
   |||:|
zb 8 KGLVRQLQFR 18

RESULT 20
US-09-328-352-4261
; Sequence 4261, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4261
; LENGTH: 434
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4261

Query Match      64.3%; Score 36; DB 2; Length 434;
Best Local Similarity 58.3%; Pred. No. 1.7e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLR 12
   |||:|
Db 51 KALVQEQRQVQ 62

Search completed: April 14, 2006, 13:15:04
Job time : 49 secs

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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 14, 2006, 13:14:28 ; Search time 172 Seconds  
(without alignments)  
29.151 Million cell updates/sec

Title: US-09-991-809-1

Perfect score: 56  
Sequence: 1 KALVQOMEQLRQ 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA\_Main:  
1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep.\*  
3: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep.\*  
4: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*  
6: /cgn2\_6/ptodata/1/pubpaa/US11\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	12	3	US-09-991-809-1
2	56	100.0	396	3	US-09-800-729-207
3	56	100.0	396	3	US-09-987-107-33
4	56	100.0	396	5	US-10-741-600-1631
5	56	100.0	396	6	US-11-017-037-33
6	56	100.0	396	6	US-11-017-059-33
7	56	100.0	397	5	US-10-656-053B-123
8	56	100.0	401	3	US-09-987-107-36
9	56	100.0	401	5	US-10-987-454-29
10	56	100.0	401	5	US-10-987-454-32
11	56	100.0	401	6	US-11-017-037-36
12	56	100.0	401	6	US-11-017-059-36
13	56	100.0	429	3	US-09-987-107-34
14	56	100.0	429	5	US-10-987-454-30
15	56	100.0	429	6	US-11-017-037-34
16	56	100.0	429	6	US-11-017-059-34
17	51	91.1	91	5	US-10-987-454-31
18	51	91.1	396	3	US-09-802-640-16
19	51	91.1	396	4	US-10-403-902A-16
20	51	91.1	396	5	US-10-741-600-1632
21	51	91.1	396	5	US-10-987-454-7
22	49	87.5	375	5	US-10-987-454-26
23	49	87.5	391	3	US-09-800-729-208
24	49	87.5	395	3	US-09-987-107-35
25	49	87.5	395	6	US-11-017-037-35
26	49	87.5	395	6	US-11-017-059-35
27	49	87.5	435	5	US-10-987-454-27

28	47	83.9	382	3	US-09-800-729-206	Sequence 206, App
29	47	83.9	382	3	US-09-987-107-37	Sequence 37, Appl
30	47	83.9	382	5	US-10-987-454-28	Sequence 28, Appl
31	47	83.9	382	6	US-11-017-037-37	Sequence 37, Appl
32	47	83.9	382	6	US-11-017-059-37	Sequence 37, Appl
33	46	82.1	10	3	US-09-791-378-561	Sequence 561, App
34	46	82.1	10	3	US-09-826-290-317	Sequence 317, App
35	46	82.1	10	3	US-09-826-290-333	Sequence 333, App
36	46	82.1	10	3	US-09-826-290-424	Sequence 424, App
37	46	82.1	10	3	US-09-791-393-226	Sequence 226, App
38	46	82.1	10	3	US-09-791-389-226	Sequence 226, App
39	46	82.1	10	3	US-09-791-377-561	Sequence 561, App
40	46	82.1	10	4	US-10-264-309-25	Sequence 25, Appl
41	46	82.1	10	4	US-10-601-100-65	Sequence 65, Appl
42	46	82.1	10	4	US-10-700-340-12	Sequence 12, Appl
43	46	82.1	10	5	US-10-264-309-25	Sequence 25, Appl
44	43	76.8	391	3	US-09-987-107-38	Sequence 38, Appl
45	43	76.8	391	4	US-10-316-253-238	Sequence 238, App

ALIGNMENTS

RESULT 1  
US-09-991-809-1  
; Sequence 1, Application US/09991809  
; Publication No. US20030100014A1  
; GENERAL INFORMATION:  
; APPLICANT: Jackowski, George  
; TITLE OF INVENTION: Apolipoprotein Biopolymer Markers Predictive of Type II Diabetes  
; FILE REFERENCE: 2132.111  
; CURRENT APPLICATION NUMBER: US/09/991.809  
; CURRENT FILING DATE: 2001-11-23  
; NUMBER OF SEQ ID NOS: 4  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-991-809-1

Query Match 100.0%; Score 56; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.0077;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12  
Db 1 KALVQOMEQLRQ 12

RESULT 2  
US-09-800-729-207  
; Sequence 207, Application US/09800729  
; Patent No. US20020068319A1  
; GENERAL INFORMATION:  
; APPLICANT: Ni et al.  
; TITLE OF INVENTION: 32 Human secreted proteins  
; FILE REFERENCE: PZ044P1  
; CURRENT APPLICATION NUMBER: US/09/800.729  
; CURRENT FILING DATE: 2001-03-08  
; PRIOR APPLICATION NUMBER: PCT/US00/26013  
; PRIOR FILING DATE: 2000-09-22  
; PRIOR APPLICATION NUMBER: 60/155,709  
; PRIOR FILING DATE: 1999-09-24  
; NUMBER OF SEQ ID NOS: 217  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 207  
; LENGTH: 396  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-800-729-207

Query Match 100.0%; Score 56; DB 3; Length 396;

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Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KALVQOMEQLRQ 12
DB 316 KALVQOMEQLRQ 327

RESULT 3
US-09-987-107-33
; Sequence 33, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-987-107-33

Query Match 100.0%; Score 56; DB 3; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KALVQOMEQLRQ 12
DB 316 KALVQOMEQLRQ 327

RESULT 4
US-10-741-600-1631
; Sequence 1631, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CL001499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 7397
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1631
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1631

Query Match 100.0%; Score 56; DB 5; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KALVQOMEQLRQ 12
DB 316 KALVQOMEQLRQ 327

RESULT 5
US-11-017-037-33
; Sequence 33, Application US/11017037
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Publication No. US20050096277A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/11/017,037
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-017-037-33

Query Match 100.0%; Score 56; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KALVQOMEQLRQ 12
DB 316 KALVQOMEQLRQ 327

RESULT 6
US-11-017-059-33
; Sequence 33, Application US/11017059
; Publication No. US20050142639A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/11/017,059
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-017-059-33

Query Match 100.0%; Score 56; DB 6; Length 396;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KALVQOMEQLRQ 12
DB 316 KALVQOMEQLRQ 327

RESULT 7
US-10-656-053B-123
; Sequence 123, Application US/10656053B
; Publication No. US20050215499A1
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; GENERAL INFORMATION:  
 ; APPLICANT: GUEVERA, JR., JUAN G.  
 ; APPLICANT: HOOGEVEEN, RON C.  
 ; APPLICANT: MOORE, PAUL J.  
 ; TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID VECTORS  
 ; FILE REFERENCE: ARAG-003USD1  
 ; CURRENT APPLICATION NUMBER: US/10/656,053B  
 ; CURRENT FILING DATE: 2003-09-05  
 ; PRIOR APPLICATION NUMBER: 09/079,030  
 ; PRIOR FILING DATE: 1998-05-14  
 ; PRIOR APPLICATION NUMBER: 08/874,807  
 ; PRIOR FILING DATE: 1997-06-13  
 ; NUMBER OF SEQ ID NOS: 229  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 123  
 ; LENGTH: 397  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-656-053B-123

Query Match 100.0%; Score 56; DB 5; Length 397;  
 Best Local Similarity 100.0%; Pred. No. 0.28;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12  
 Db 317 KALVQOMEQLRQ 328

RESULT 8  
 US-09-987-107-36  
 ; Sequence 36, Application US/09987107  
 ; Patent No. US20020156007A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GRAVERSEN, Jonas  
 ; APPLICANT: MOESTRUP, Soren  
 ; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES  
 ; FILE REFERENCE: GRAVERSEN1A  
 ; CURRENT APPLICATION NUMBER: US/09/987,107  
 ; CURRENT FILING DATE: 2001-11-13  
 ; PRIOR APPLICATION NUMBER: US 60/264,022  
 ; PRIOR FILING DATE: 2001-01-26  
 ; PRIOR APPLICATION NUMBER: DK PA2001 00057  
 ; PRIOR FILING DATE: 2001-01-15  
 ; PRIOR APPLICATION NUMBER: DK PA2000 01682  
 ; PRIOR FILING DATE: 2000-11-10  
 ; NUMBER OF SEQ ID NOS: 91  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 36  
 ; LENGTH: 401  
 ; TYPE: PRT  
 ; ORGANISM: Papio anubis  
 US-09-987-107-36

Query Match 100.0%; Score 56; DB 3; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 0.28;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12  
 Db 300 KALVQOMEQLRQ 311

RESULT 9  
 US-10-987-454-29  
 ; Sequence 29, Application US/10987454  
 ; Publication No. US20050172359A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Reid, Alexandra  
 ; APPLICANT: Moloney, Maurice  
 ; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF APOLIPOPROTEINS IN TRANSGENIC  
 ; FILE REFERENCE: 9369-311

; CURRENT APPLICATION NUMBER: US/10/987,454  
 ; CURRENT FILING DATE: 2004-11-15  
 ; PRIOR APPLICATION NUMBER: US 60/519,606  
 ; PRIOR FILING DATE: 2003-11-14  
 ; PRIOR APPLICATION NUMBER: US 60/579,733  
 ; PRIOR FILING DATE: 2004-06-16  
 ; NUMBER OF SEQ ID NOS: 251  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 29  
 ; LENGTH: 401  
 ; TYPE: PRT  
 ; ORGANISM: Papio anubis  
 US-10-987-454-29

Query Match 100.0%; Score 56; DB 5; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 0.28;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12  
 Db 300 KALVQOMEQLRQ 311

RESULT 10  
 US-10-987-454-32  
 ; Sequence 32, Application US/10987454  
 ; Publication No. US20050172359A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Reid, Alexandra  
 ; APPLICANT: Moloney, Maurice  
 ; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF APOLIPOPROTEINS IN TRANSGENIC  
 ; FILE REFERENCE: 9369-311  
 ; CURRENT APPLICATION NUMBER: US/10/987,454  
 ; CURRENT FILING DATE: 2004-11-15  
 ; PRIOR APPLICATION NUMBER: US 60/519,606  
 ; PRIOR FILING DATE: 2003-11-14  
 ; PRIOR APPLICATION NUMBER: US 60/579,733  
 ; PRIOR FILING DATE: 2004-06-16  
 ; NUMBER OF SEQ ID NOS: 251  
 ; SOFTWARE: PatentIn version 3.3  
 ; SEQ ID NO 32  
 ; LENGTH: 401  
 ; TYPE: PRT  
 ; ORGANISM: Papio sp.  
 US-10-987-454-32

Query Match 100.0%; Score 56; DB 5; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 0.28;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12  
 Db 300 KALVQOMEQLRQ 311

RESULT 11  
 US-11-017-037-36  
 ; Sequence 36, Application US/11017037  
 ; Publication No. US20050096277A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GRAVERSEN, Jonas  
 ; APPLICANT: MOESTRUP, Soren  
 ; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES  
 ; FILE REFERENCE: GRAVERSEN1A  
 ; CURRENT APPLICATION NUMBER: US/11/017,037  
 ; CURRENT FILING DATE: 2004-12-21  
 ; PRIOR APPLICATION NUMBER: US/09/987,107  
 ; PRIOR FILING DATE: 2001-11-13  
 ; PRIOR APPLICATION NUMBER: US 60/264,022  
 ; PRIOR FILING DATE: 2001-01-26  
 ; PRIOR APPLICATION NUMBER: DK PA2001 00057  
 ; PRIOR FILING DATE: 2001-01-15

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; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Papio anubis
US-11-017-037-36

Query Match      100.0%; Score 56; DB 6; Length 401;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12
Db 300 KALVQOMEQLRQ 311

RESULT 12
US-11-017-059-36
; Sequence 36, Application US/11017059
; Publication No. US20050142639A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/11/017,059
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Papio anubis
US-11-017-059-36

Query Match      100.0%; Score 56; DB 6; Length 401;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12
Db 300 KALVQOMEQLRQ 311

RESULT 13
US-09-987-107-34
; Sequence 34, Application US/09987107
; Patent No. US20020156007A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/09/987,107
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91

; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 429
; TYPE: PRT

; QUERY MATCH: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-09-987-107-34

Query Match      100.0%; Score 56; DB 3; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12
Db 316 KALVQOMEQLRQ 327

RESULT 14
US-10-987-454-30
; Sequence 30, Application US/10987454
; Publication No. US20050172359A1
; GENERAL INFORMATION:
; APPLICANT: Reid, Alexandra
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF APOLIPOPROTEINS IN TRANSGENIC
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 9369-311
; CURRENT APPLICATION NUMBER: US/10/987,454
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/519,606
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US 60/579,733
; PRIOR FILING DATE: 2004-06-16
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 30
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-10-987-454-30

Query Match      100.0%; Score 56; DB 5; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12
Db 316 KALVQOMEQLRQ 327

RESULT 15
US-11-017-037-34
; Sequence 34, Application US/11017037
; Publication No. US20050096277A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/11/017,037
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/09/987,107
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/264,022
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: DK PA2001 00057
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: DK PA2000 01682
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 429
; TYPE: PRT
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; ORGANISM: Macaca fascicularis
US-11-017-037-34
Query Match      100.0%; Score 56; DB 6; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12
Db 316 KALVQOMEQLRQ 327

RESULT 16
US-11-017-059-34
; Sequence 34, Application US/11017059
; Publication No. US20050142639A1
; GENERAL INFORMATION:
; APPLICANT: GRAVERSEN, Jonas
; APPLICANT: MOESTRUP, Soren
; TITLE OF INVENTION: APOLIPOPROTEINS ANALOGUES
; FILE REFERENCE: GRAVERSENIA
; CURRENT APPLICATION NUMBER: US/11/017,059
; CURRENT FILING DATE: 2004-12-21
; PRIOR FILING DATE: 2001-11-13
; PRIOR FILING DATE: 2001-11-13
; PRIOR FILING DATE: 2001-01-26
; PRIOR FILING DATE: 2001-01-26
; PRIOR FILING DATE: 2001-01-15
; PRIOR FILING DATE: 2001-01-15
; PRIOR FILING DATE: 2000-11-10
; PRIOR FILING DATE: 2000-11-10
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34
; LENGTH: 429
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-11-017-059-34

* Query Match      100.0%; Score 56; DB 6; Length 429;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12
Db 316 KALVQOMEQLRQ 327

RESULT 17
US-10-987-454-31
; Sequence 31, Application US/10987454
; Publication No. US20050172359A1
; GENERAL INFORMATION:
; APPLICANT: Reid, Alexandra
; APPLICANT: Moloney, Maurice
; TITLE OF INVENTION: METHODS FOR THE PRODUCTION OF APOLIPOPROTEINS IN TRANSGENIC
; TITLE OF INVENTION: PLANTS
; FILE REFERENCE: 9369-311
; CURRENT APPLICATION NUMBER: US/10/987,454
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/519,606
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US 60/579,733
; PRIOR FILING DATE: 2004-06-16
; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Pan troglodytes
US-10-987-454-31

Query Match      91.1%; Score 51; DB 5; Length 91;

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Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLR 11
Db 11 KALVQOMEQLR 21

RESULT 18
US-09-802-640-16
; Sequence 16, Application US/09802640
; Publication No. US20030036057A1
; GENERAL INFORMATION:
; APPLICANT: Braun, Andreas
; APPLICANT: Bonsal, Aruna
; APPLICANT: Klevn, Patrick
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
; FILE REFERENCE: 24736-2048
; CURRENT APPLICATION NUMBER: US/09/802,640
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-802-640-16

Query Match      91.1%; Score 51; DB 3; Length 396;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLR 11
Db 316 KALVQOMEQLR 326

RESULT 19
US-10-403-902A-16
; Sequence 16, Application US/10403902A
; Publication No. US20030224418A1
; GENERAL INFORMATION:
; APPLICANT: Braun, Andreas
; APPLICANT: Bansal, Aruna
; APPLICANT: Klevn, Patrick
; TITLE OF INVENTION: GENES AND POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE AND THEIR USE
; FILE REFERENCE: 24736-2048B
; CURRENT APPLICATION NUMBER: US/10/403,902A
; CURRENT FILING DATE: 2003-07-21
; PRIOR APPLICATION NUMBER: 09/802,640
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-403-902A-16

Query Match      91.1%; Score 51; DB 4; Length 396;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLR 11
Db 316 KALVQOMEQLR 326

RESULT 20
US-10-741-600-1632
; Sequence 1632, Application US/10741600

```

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; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1632
; LENGTH: 396
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1632
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Query Match      91.1%; Score 51; DB 5; Length 396;
Best Local Similarity 100.0%; Pred.No. 1.9;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 KALVQOMEQLR 11
        |||||
Db      316 KALVQOMEQLR 326
```

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Search completed: April 14, 2006, 13:18:03
Job time : 173 secs
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GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 14, 2006, 13:15:19 ; Search time 27 Seconds  
(without alignments)  
18.884 Million cell updates/sec

Title: US-09-991-809-1

Perfect score: 56

Sequence: 1 KALVQOMEQLRQ 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA\_New\*

- 1: /SID85/prodata/2/pubpaa/US08\_NEW\_PUB.pdb\*
- 2: /SID85/prodata/2/pubpaa/US06\_NEW\_PUB.pdb\*
- 3: /SID85/prodata/2/pubpaa/US07\_NEW\_PUB.pdb\*
- 4: /SID85/prodata/2/pubpaa/PCT\_NEW\_PUB.pdb\*
- 5: /SID85/prodata/2/pubpaa/US09\_NEW\_PUB.pdb\*
- 6: /SID85/prodata/2/pubpaa/US10\_NEW\_PUB.pdb\*
- 7: /SID85/prodata/2/pubpaa/US11\_NEW\_PUB.pdb\*
- 8: /SID85/prodata/2/pubpaa/US60\_NEW\_PUB.pdb\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	396	6	US-10-995-561-1005
2	39	69.6	311	6	US-10-055-877-181
3	39	69.6	311	6	US-10-055-877-182
4	38	67.9	498	7	US-11-072-512-3191
5	37	66.1	277	6	US-10-204-639-46
6	36	64.3	208	7	US-11-123-701-2
7	35	62.5	435	7	US-11-087-099-11022
8	35	62.5	565	6	US-10-485-517-300
9	35	62.5	593	7	US-11-051-720-1343
10	35	62.5	608	7	US-11-098-686-10813
11	35	62.5	674	7	US-11-051-720-1342
12	35	62.5	725	7	US-11-051-720-1341
13	35	62.5	737	7	US-11-051-720-1345
14	35	62.5	911	6	US-10-330-773-712
15	35	62.5	952	6	US-10-330-773-709
16	35	62.5	957	7	US-11-051-720-1438
17	35	62.5	5024	6	US-10-793-626-2964
18	34	60.7	206	7	US-11-087-099-2672
19	34	60.7	206	7	US-11-188-298-13569
20	34	60.7	208	6	US-10-055-877-186
21	34	60.7	242	7	US-11-087-099-2658
22	34	60.7	356	6	US-10-055-877-184
23	34	60.7	356	6	US-10-055-877-185
24	34	60.7	488	7	US-11-188-298-16569
25	34	60.7	1110	7	US-11-079-463-6048

26	34	60.7	1411	6	US-10-453-372-1106	Sequence 1106, Ap
27	34	60.7	1593	6	US-10-453-372-1092	Sequence 1092, Ap
28	33	58.9	262	7	US-11-096-568A-26468	Sequence 26468, A
29	33	58.9	269	7	US-11-172-740-483	Sequence 483, App
30	33	58.9	284	6	US-10-131-826A-118	Sequence 118, App
31	33	58.9	284	6	US-10-973-115B-118	Sequence 118, App
32	33	58.9	284	6	US-11-290-153-118	Sequence 118, App
33	33	58.9	323	7	US-11-096-568A-2168	Sequence 2168, App
34	33	58.9	349	7	US-11-096-568A-2167	Sequence 2167, Ap
35	33	58.9	375	7	US-11-096-568A-2166	Sequence 2166, Ap
36	33	58.9	399	7	US-11-096-568A-26467	Sequence 26467, A
37	33	58.9	439	7	US-11-096-568A-26466	Sequence 26466, A
38	33	58.9	466	7	US-11-087-099-1606	Sequence 1606, Ap
39	33	58.9	544	7	US-11-188-298-6393	Sequence 6393, Ap
40	33	58.9	1089	7	US-11-098-686-10150	Sequence 10150, A
41	33	58.9	1976	7	US-11-069-834-52	Sequence 52, Appl
42	33	58.9	1976	7	US-11-069-834-54	Sequence 54, Appl
43	33	58.9	1992	7	US-11-069-834-58	Sequence 58, Appl
44	33	58.9	2000	7	US-11-069-834-56	Sequence 56, Appl
45	32	57.1	68	7	US-11-120-308-142	Sequence 142, App

#### ALIGNMENTS

##### RESULT 1

US-10-995-561-1005  
; Sequence 1005, Application US/10995561  
; Publication No. US20050272054A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 2004-11-24  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 1005  
; LENGTH: 396  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-995-561-1005

Query Match 100.0% Score 56; DB 6; Length 396;  
Best Local Similarity 100.0%; Pred. No. 0.018;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12  
Db 316 KALVQOMEQLRQ 327

##### RESULT 2

US-10-055-877-181  
; Sequence 181, Application US/10055877  
; Publication No. US20050288241A1  
; GENERAL INFORMATION:  
; APPLICANT: Decristofaro, Marc  
; APPLICANT: Padigaru, Muralidhara  
; APPLICANT: Miller, Charles  
; APPLICANT: Tchernev, Velizar  
; APPLICANT: Zhong, Mei  
; APPLICANT: Anderson, David  
; APPLICANT: Ballinger, Robert  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Ratelli, Luca  
; APPLICANT: Ketuda, Ramesh  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Zerhusen, Bryan  
; APPLICANT: Andrew, David

```

; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eisen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shimkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ference
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 181
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Coturnix coturnix
US-10-055-877-181

```

```

Query Match          69.6%; Score 39; DB 6; Length 311;
Best Local Similarity 70.0%; Pred. No. 13;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      3 LVQQMEQLRQ 12
      |:|:|:|:|:|
Db      261 LIQQVEQLKQ 270

```

```

RESULT 3
US-10-055-877-182
; Sequence 182, Application US/10055877
; Publication No. US20050288241A1
; GENERAL INFORMATION:
; APPLICANT: DeCristofaro, Marc
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Miller, Charles
; APPLICANT: Tchernev, Velizar
; APPLICANT: Zhong, Mei
; APPLICANT: Anderson, David
; APPLICANT: Ballinger, Robert
; APPLICANT: Gerlach, Valerie
; APPLICANT: Spytek, Kimberly
; APPLICANT: Ratelli, Luca
; APPLICANT: Kekuda, Ramesh

```

```

; APPLICANT: Guo, Xiaojia
; APPLICANT: Zerhusen, Bryan
; APPLICANT: Andrew, David
; APPLICANT: Mezes, Peter
; APPLICANT: Patturajan, Meera
; APPLICANT: Burgess, Catherine
; APPLICANT: Eisen, Andrew
; APPLICANT: Wolenc, Adam
; APPLICANT: Baumgartner, Jason
; APPLICANT: Shimkets, Richard
; APPLICANT: Gusev, Vladimir
; APPLICANT: Vernet, Corine
; APPLICANT: Taupier Jr., Raymond
; APPLICANT: Pena, Carol
; APPLICANT: Shenoy, Suresh
; APPLICANT: Li, Li
; APPLICANT: Casman, Stacie
; APPLICANT: Boldog, Ference
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby
; FILE REFERENCE: 21402-251
; CURRENT APPLICATION NUMBER: US/10/055,877
; CURRENT FILING DATE: 2002-01-22
; PRIOR APPLICATION NUMBER: 60/262,892
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: 60/263,598
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 60/263,799
; PRIOR FILING DATE: 2001-01-24
; PRIOR APPLICATION NUMBER: 60/264,117
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,139
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 60/264,478
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/263,351
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: 60/272,870
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/275,990
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: 60/275,927
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 512
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 182
; LENGTH: 311
; TYPE: PRT
; ORGANISM: Gallus gallus
US-10-055-877-182

```

```

Query Match          69.6%; Score 39; DB 6; Length 311;
Best Local Similarity 70.0%; Pred. No. 13;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      3 LVQQMEQLRQ 12
      |:|:|:|:|:|
Db      261 LIQQVEQLKQ 270

```

```

RESULT 4
US-11-072-512-3191
; Sequence 3191, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO

```

RESULT 6  
US-11-123-701-2  
; Sequence 2, Application US/111233701

; CURRENT APPLICATION NUMBER: US/10/485,517  
; CURRENT FILING DATE: 2004-02-02  
; PRIOR APPLICATION NUMBER: GB 0118825.9  
; PRIOR FILING DATE: 2001-08-02  
; PRIOR APPLICATION NUMBER: GB 0200349.9  
; PRIOR FILING DATE: 2002-01-09  
; NUMBER OF SEQ ID NOS: 424  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 300  
; LENGTH: 565  
; TYPE: PRT  
; ORGANISM: Staphylococcus aureus  
US-10-485-517-300

Query Match 62.5%; Score 35; DB 6; Length 565;  
Best Local Similarity 70.0%; Pred. No. 1.3e+02;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 LVQOMEQLRQ 12  
|:|:|||||  
Db 375 LLQMEQLEQ 384

RESULT 9

US-11-051-720-1343  
; Sequence 1343, Application US/11051720  
; Publication No. US20060046257A1  
; GENERAL INFORMATION:  
; APPLICANT: Compugen Ltd  
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS  
; FILE REFERENCE: 1847.1002  
; CURRENT APPLICATION NUMBER: US/11/051,720  
; CURRENT FILING DATE: 2005-01-27  
; NUMBER OF SEQ ID NOS: 1780  
; SEQ ID NO 1343  
; LENGTH: 593  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-051-720-1343

Query Match 62.5%; Score 35; DB 7; Length 593;  
Best Local Similarity 66.7%; Pred. No. 1.4e+02;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12  
||| |||||  
Db 337 KALEQQMESHRE 348

RESULT 10

US-11-098-686-10813  
; Sequence 10813, Application US/11098686  
; Publication No. US20060024696A1  
; GENERAL INFORMATION:  
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.  
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES  
; FILE REFERENCE: 09531-128001  
; CURRENT APPLICATION NUMBER: US/11/098,686  
; CURRENT FILING DATE: 2005-04-04  
; PRIOR APPLICATION NUMBER: PCT/US03/31318  
; PRIOR FILING DATE: 2003-10-01  
; PRIOR APPLICATION NUMBER: US 60/416,395  
; PRIOR FILING DATE: 2002-10-04  
; NUMBER OF SEQ ID NOS: 11433  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10813  
; LENGTH: 608  
; TYPE: PRT  
; ORGANISM: Lawsonia intracellularis  
US-11-098-686-10813

Query Match 62.5%; Score 35; DB 7; Length 608;  
Best Local Similarity 70.0%; Pred. No. 1.4e+02;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ALVQOMEQLR 11  
|:|:|||||  
Db 512 ALQQMDSLR 521

RESULT 11

US-11-051-720-1342  
; Sequence 1342, Application US/11051720  
; Publication No. US20060046257A1  
; GENERAL INFORMATION:  
; APPLICANT: Compugen Ltd  
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS  
; FILE REFERENCE: 1847.1002  
; CURRENT APPLICATION NUMBER: US/11/051,720  
; CURRENT FILING DATE: 2005-01-27  
; NUMBER OF SEQ ID NOS: 1780  
; SEQ ID NO 1342  
; LENGTH: 674  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-051-720-1342

Query Match 62.5%; Score 35; DB 7; Length 674;  
Best Local Similarity 66.7%; Pred. No. 1.6e+02;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12  
||| |||||  
Db 418 KALEQQMESHRE 429

RESULT 12

US-11-051-720-1341  
; Sequence 1341, Application US/11051720  
; Publication No. US20060046257A1  
; GENERAL INFORMATION:  
; APPLICANT: Compugen Ltd  
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS  
; FILE REFERENCE: 1847.1002  
; CURRENT APPLICATION NUMBER: US/11/051,720  
; CURRENT FILING DATE: 2005-01-27  
; NUMBER OF SEQ ID NOS: 1780  
; SEQ ID NO 1341  
; LENGTH: 725  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-051-720-1341

Query Match 62.5%; Score 35; DB 7; Length 725;  
Best Local Similarity 66.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12  
||| |||||  
Db 469 KALEQQMESHRE 480

RESULT 13

US-11-051-720-1345  
; Sequence 1345, Application US/11051720  
; Publication No. US20060046257A1  
; GENERAL INFORMATION:  
; APPLICANT: Compugen Ltd  
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS  
; FILE REFERENCE: 1847.1002  
; CURRENT APPLICATION NUMBER: US/11/051,720

; CURRENT FILING DATE: 2005-01-27  
; NUMBER OF SEQ ID NOS: 1780  
; SEQ ID NO 1345  
; LENGTH: 737  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-051-720-1345

Query Match 62.5%; Score 35; DB 7; Length 737;  
Best Local Similarity 66.7%; Pred. No. 1.7e+02;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12  
||| ||||| |  
Db 701 KALEQQMESHRE 712

## RESULT 14

US-10-330-773-712  
; Sequence 712, Application US/10330773  
; Publication No. US20060040262A1  
; GENERAL INFORMATION:  
; APPLICANT: David W. Morris  
; APPLICANT: Marc Malandro  
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer  
; FILE REFERENCE: 529452001300  
; CURRENT APPLICATION NUMBER: US/10/330,773  
; CURRENT FILING DATE: 2002-12-27  
; NUMBER OF SEQ ID NOS: 981  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 712  
; LENGTH: 911  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-330-773-712

Query Match 62.5%; Score 35; DB 6; Length 911;  
Best Local Similarity 66.7%; Pred. No. 2.2e+02;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12  
||| ||||| |  
Db 655 KALEQQMESHRE 666

## RESULT 15

US-10-330-773-709  
; Sequence 709, Application US/10330773  
; Publication No. US20060040262A1  
; GENERAL INFORMATION:  
; APPLICANT: David W. Morris  
; APPLICANT: Marc Malandro  
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer  
; FILE REFERENCE: 529452001300  
; CURRENT APPLICATION NUMBER: US/10/330,773  
; CURRENT FILING DATE: 2002-12-27  
; NUMBER OF SEQ ID NOS: 981  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 709  
; LENGTH: 952  
; TYPE: PRT  
; ORGANISM: Mus musculus  
US-10-330-773-709

Query Match 62.5%; Score 35; DB 6; Length 952;  
Best Local Similarity 66.7%; Pred. No. 2.3e+02;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12  
||| ||||| |  
Db 696 KALEQQMESHRE 707

## RESULT 16

US-11-051-720-1438  
; Sequence 1438, Application US/11051720  
; Publication No. US20060046257A1  
; GENERAL INFORMATION:  
; APPLICANT: Compugen Ltd  
; TITLE OF INVENTION: NOVEL NUCLEOTIDE AND AMINO ACID SEQUENCES, AND ASSAYS AND METHODS  
; FILE REFERENCE: 1847.1002  
; CURRENT APPLICATION NUMBER: US/11/051,720  
; CURRENT FILING DATE: 2005-01-27  
; NUMBER OF SEQ ID NOS: 1780  
; SEQ ID NO 1438  
; LENGTH: 957  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-11-051-720-1438

Query Match 62.5%; Score 35; DB 7; Length 957;  
Best Local Similarity 66.7%; Pred. No. 2.4e+02;  
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12  
||| ||||| |  
Db 701 KALEQQMESHRE 712

## RESULT 17

US-10-793-626-2964  
; Sequence 2964, Application US/10793626  
; Publication No. US20050255478A1  
; GENERAL INFORMATION:  
; APPLICANT: KIMMERLY, WILLIAM JOHN  
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
; FILE REFERENCE: PU3480US  
; CURRENT APPLICATION NUMBER: US/10/793,626  
; CURRENT FILING DATE: 2004-03-04  
; PRIOR APPLICATION NUMBER: 60/164,258  
; PRIOR FILING DATE: 1999-11-09  
; NUMBER OF SEQ ID NOS: 4472  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2964  
; LENGTH: 5024  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: synthetic  
; OTHER INFORMATION: amino acid sequence  
; FEATURE:  
; NAME/KEY: MOD RES  
; LOCATION: (5024)  
; OTHER INFORMATION: variable amino acid  
US-10-793-626-2964

Query Match 62.5%; Score 35; DB 6; Length 5024;  
Best Local Similarity 58.3%; Pred. No. 1.6e+03;  
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12  
||| ||||| |  
Db 2007 KAINQAMQQLKQ 2018

## RESULT 18

US-11-087-099-2672  
; Sequence 2672, Application US/11087099  
; Publication No. US20060041961A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: Genes and Uses for Plant Improvement  
; FILE REFERENCE: 38-21(53450)B EP  
; CURRENT APPLICATION NUMBER: US/11/087,099  
; CURRENT FILING DATE: 2005-03-22

; NUMBER OF SEQ ID NOS: 12464  
; SEQ ID NO 2672  
; LENGTH: 206  
; TYPE: PRT  
; ORGANISM: Michelia figo  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(206)  
; OTHER INFORMATION: unsure at all Xaa locations  
US-11-087-099-2672

Query Match 60.7%; Score 34; DB 7; Length 206;  
Best Local Similarity 50.0%; Pred. No. 61;  
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 LVQQMEQLRQ 12  
:::|||||:  
Db 140 MIEQMEELRK 149

## RESULT 19

US-11-188-298-13569  
; Sequence 13569, Application US/11188298  
; Publication No. US20060075522A1  
; GENERAL INFORMATION:  
; APPLICANT: Abad, Mark S. et al.  
; TITLE OF INVENTION: GENES AND USES FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-21(53452)B  
; CURRENT APPLICATION NUMBER: US/11/188,298  
; CURRENT FILING DATE: 2005-07-22  
; PRIOR APPLICATION NUMBER: 60/592,978  
; PRIOR FILING DATE: 2004-07-31  
; NUMBER OF SEQ ID NOS: 22569  
; SEQ ID NO 13569  
; LENGTH: 206  
; TYPE: PRT  
; ORGANISM: Michelia figo  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(206)  
; OTHER INFORMATION: unsure at all Xaa locations  
US-11-188-298-13569

Query Match 60.7%; Score 34; DB 7; Length 206;  
Best Local Similarity 50.0%; Pred. No. 61;  
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 3 LVQQMEQLRQ 12  
:::|||||:  
Db 140 MIEQMEELRK 149

## RESULT 20

US-10-055-877-186  
; Sequence 186, Application US/10055877  
; Publication No. US20050288241A1  
; GENERAL INFORMATION:  
; APPLICANT: DeCristofaro, Marc  
; APPLICANT: Padigar, Muralidhara  
; APPLICANT: Miller, Charles  
; APPLICANT: Tchernev, Velizar  
; APPLICANT: Zhong, Mei  
; APPLICANT: Anderson, David  
; APPLICANT: Ballinger, Robert  
; APPLICANT: Gerlach, Valerie  
; APPLICANT: Spytek, Kimberly  
; APPLICANT: Ratelli, Luca  
; APPLICANT: Kekuda, Ramesh  
; APPLICANT: Guo, Xiaojia  
; APPLICANT: Zerhusen, Bryan  
; APPLICANT: Andrew, David  
; APPLICANT: Mezes, Peter  
; APPLICANT: Patturajan, Meera

; APPLICANT: Burgess, Catherine  
; APPLICANT: Eisen, Andrew  
; APPLICANT: Wolenc, Adam  
; APPLICANT: Baumgartner, Jason  
; APPLICANT: Shimkets, Richard  
; APPLICANT: Gusev, Vladimir  
; APPLICANT: Vernet, Corine  
; APPLICANT: Taupier Jr., Raymond  
; APPLICANT: Pena, Carol  
; APPLICANT: Shenoy, Suresh  
; APPLICANT: Li, Li  
; APPLICANT: Casman, Stacie  
; APPLICANT: Boldog, Ference  
; TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoded Thereby  
; FILE REFERENCE: 21402-251  
; CURRENT APPLICATION NUMBER: US/10/055,877  
; CURRENT FILING DATE: 2002-01-22  
; PRIOR APPLICATION NUMBER: 60/262,892  
; PRIOR FILING DATE: 2001-01-19  
; PRIOR APPLICATION NUMBER: 60/263,598  
; PRIOR FILING DATE: 2001-01-23  
; PRIOR APPLICATION NUMBER: 60/263,799  
; PRIOR FILING DATE: 2001-01-24  
; PRIOR APPLICATION NUMBER: 60/264,117  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 60/264,139  
; PRIOR FILING DATE: 2001-01-25  
; PRIOR APPLICATION NUMBER: 60/264,478  
; PRIOR FILING DATE: 2001-01-26  
; PRIOR APPLICATION NUMBER: 60/263,351  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: 60/272,870  
; PRIOR FILING DATE: 2001-03-02  
; PRIOR APPLICATION NUMBER: 60/275,990  
; PRIOR FILING DATE: 2001-03-14  
; PRIOR APPLICATION NUMBER: 60/275,927  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 512  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 186  
; LENGTH: 208  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: bZIP\_Maf  
; OTHER INFORMATION: domain consensus sequence  
US-10-055-877-186

Query Match 60.7%; Score 34; DB 6; Length 208;  
Best Local Similarity 60.0%; Pred. No. 62;  
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 LVQQMEQLRQ 12  
:::|||||:  
Db 155 LAQLEQLKE 164

Search completed: April 14, 2006, 13:18:35  
Job time : 28 secs



GenCore version 5.1.7  
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OM protein - protein search, using sw model.

Run on: April 14, 2006, 13:09:43 ; Search time 39 Seconds  
(without alignments)  
29.605 Million cell updates/sec

Title: US-09-991-809-1

Perfect score: 56

Sequence: 1 KALVQQMEQLRQ 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_80:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	396	1 LPHU44	apolipoprotein A-I
2	56	100.0	401	2 A47141	apolipoprotein A-I
3	56	100.0	429	2 S29565	apolipoprotein A-I
4	51	91.1	91	2 I54248	apolipoprotein A-I
5	49	87.5	391	2 B40892	apolipoprotein A-I
6	49	87.5	395	2 A40892	apolipoprotein A-I
7	49	87.5	399	2 C40892	apolipoprotein A-I
8	44	78.6	394	2 A25281	apolipoprotein A-I
9	43	76.8	391	1 LKRTA4	apolipoprotein A-I
10	39	69.6	311	2 A56235	transcription acti
11	39	69.6	323	2 I49529	transcription prote
12	39	69.6	2712	2 T05113	hypothetical prote
13	38	67.9	219	2 B41886	flagellar membrane
14	38	67.9	597	2 S40998	hypothetical prote
15	38	67.9	893	2 G88551	protein M01A6.2 [i
16	37	66.1	177	2 B69520	hypothetical prote
17	37	66.1	359	2 A12368	hypothetical prote
18	37	66.1	893	2 AH2007	toxin secretion AB
19	36	64.3	208	2 E75520	hypothetical prote
20	36	64.3	370	2 AG0761	probable propanol
21	36	64.3	498	2 H83880	hypothetical prote
22	36	64.3	1189	2 A54817	ATPase Scrl, chrom
23	36	64.3	1279	2 T13613	hypothetical prote
24	36	64.3	1738	2 T14867	interaptin - slime
25	36	64.3	2024	2 A54103	centrosome autout
26	35	62.5	79	2 A50012	conserved hypothet
27	35	62.5	190	2 H71245	hypothetical prote
28	35	62.5	338	2 S73441	MG032 homolog B01
29	35	62.5	394	2 E64028	hypothetical prote

RESULT 1

LPHU44

apolipoprotein A-IV precursor [validated] - human

NiAlternate names: apoA-IV

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1987 #sequence revision 30-Sep-1987 #text change 31-Dec-2004

C/Accession: A94137; A94059; A24449; A29330; A26280; I37117; C54223; A61203; A26481; S02

R/Karathanasis, S.K.; Oettgen, P.; Haddad, I.A.; Antonarakis, S.E.

Proc. Natl. Acad. Sci. U.S.A. 83, 8457-8461, 1986

A/Title: Structure, evolution, and polymorphisms of the human apolipoprotein A4 gene (AP

A/Reference number: A94137; MUID:87041474; PMID:3095836

A/Accession: A94137

A/Molecule type: DNA

A/Residues: 1-396 <KAR1>

A/Cross-references: UNIPROT:P06727; UNIPROT:Q13784; UNIPARC:UPI000016A56E; GB:M14642; NI

R/Karathanasis, S.K.

Proc. Natl. Acad. Sci. U.S.A. 82, 6374-6378, 1985

A/Title: Apolipoprotein multigene family: tandem organization of human apolipoprotein AI

A/Reference number: A94059; MUID:86016704; PMID:3931073

A/Accession: A94059

A/Molecule type: mRNA

A/Residues: 135-378 <KAR2>

A/Cross-references: UNIPARC:UPI000006D9F1; GB:M10373; NID:G563319; PIDN:AAB59516.1; PID:

R/Karathanasis, S.K.; Yunis, I.

Biochemistry 25, 3962-3970, 1986

A/Title: Structure, evolution, and tissue-specific synthesis of human apolipoprotein AIV

A/Reference number: A24449; MUID:86298629; PMID:3755616

A/Accession: A24449

A/Molecule type: mRNA

A/Residues: 1-396 <KAR3>

A/Cross-references: UNIPARC:UPI000016A56E; GB:M13654; NID:G178758; PIDN:AAA51744.1; PID

R/Gordon, J.I.; Bisgaier, C.L.; Sims, H.F.; Sachdev, O.P.; Glickman, R.M.; Strauss, A.W

J. Biol. Chem. 259, 468-474, 1984

A/Title: Biosynthesis of human preapolipoprotein A-IV.

A/Reference number: A92475; MUID:84161950; PMID:6706947

A/Contents: annotation: signal sequence cleavage site

R/Eishourbagy, N.A.; Walker, D.W.; Paik, Y.K.; Boguski, M.S.; Freeman, M.; Gordon, J.I.,

J. Biol. Chem. 262, 7973-7981, 1987

A/Title: Structure and expression of the human apolipoprotein A-IV gene.

A/Reference number: A29330; MUID:87250378; PMID:3036793

A/Accession: A29330

A/Molecule type: DNA

A/Residues: 1-157, 'T', 159, 'Y', 161-278, 'R', 280-326, 'T', 328-379, 'H', 381-396 <ELS>

A/Cross-references: UNIPARC:UPI00001678CB; GB:J02758; NID:G178756; PIDN:AAA96731.1; PID:

R/Eishourbagy, N.A.; Walker, D.W.; Boguski, M.S.; Gordon, J.I.; Taylor, J.M.

J. Biol. Chem. 261, 1998-2002, 1986

A/Title: The nucleotide and derived amino acid sequence of human apolipoprotein A-IV mRNA

A/Reference number: A26280; MUID:86111885; PMID:3080432

A/Accession: A26280

A/Molecule type: mRNA

A/Residues: 21-157, 'T', 159, 'Y', 161-278, 'R', 280-326, 'T', 328-379, 'H', 381-396 <EL2>

A/Cross-references: UNIPARC:UPI000016A56F; GB:M14566; NID:G178778; PIDN:AAA51748.1; PID:

R;Yang, C.Y.; Gu, Z.W.; Chong, I.S.; Xiong, W.J.; Rosseneu, M.; Yang, H.X.; Lee, B.R.; C  
Biochim. Biophys. Acta 1002, 231-237, 1989  
A;Title: The primary structure of human apolipoprotein A-IV.  
A;Reference number: 137177; PMID:89194198; PMID:2930771  
A;Accession: 137177  
A;Status: translated from GB/EMBL/DBDJ  
A;Molecule type: mRNA  
A;Residues: 1-157, 'T', 159, 'Y', 161-278, 'R', 280-396 <YAN1>  
A;Cross-references: UNIPARC:UPI000013CBBD; EMBL:X13629; NID:g28761; PIDN:CAA31955.1; PID  
A;Note: submitted to the EMBL Data Library, January 1989  
R;Kunitake, S.T.; Carilli, C.T.; Lau, K.; Protter, A.A.; Naya-Vigne, J.; Kane, J.P.  
Biochemistry 33, 1988-1993, 1994  
A;Title: Identification of proteins associated with apolipoprotein A-I-containing lipop  
A;Reference number: A54223; PMID:94162201; PMID:8117655  
A;Accession: C54223  
A;Molecule type: protein  
A;Residues: 'X', 22, 'X', 24, 'X', 26-31, 'X', 33-34 <KUN>  
A;Cross-references: UNIPARC:UPI0000174029  
R;Tenkanen, H.; Lukka, M.; Jauhainen, M.; Metso, J.; Baumann, M.; Peltonen, L.; Ehnholm  
Arterioscler. Thromb. 11, 851-856, 1991  
A;Title: The mutation causing the common apolipoprotein A-IV polymorphism is a glutamine  
A;Reference number: A61203; PMID:91291788; PMID:2065039  
A;Accession: A61203  
A;Status: not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 378-379, 'H', 381-382 <TEN>  
A;Cross-references: UNIPARC:UPI000017402A  
C;Comment: ApoA-IV is a major lipoprotein of lymph chylomicrons. In human plasma, it is  
C;Comment: ApoA-IV is synthesized primarily in the intestine.  
C;Genetics:  
A;Gene: GDB:AP0A4  
A;Cross-references: GDB:119000; OMIM:107690  
A;Map position: 11q23-11q23  
A;Introns: 17/1; 59/2  
C;Keywords: chylomicron; HDL; intestine; lipid binding; lipid transport; lipoprotein; pl  
F;1-20/Domain: signal sequence #status experimental <SIG>  
F;21-396/Product: apolipoprotein A-IV #status experimental <MAT>  
  
Query Match 100.0%; Score 56; DB 1; Length 396;  
Best Local Similarity 100.0%; Pred. No. 0.04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 KALVQOMEQLRQ 12  
Db 316 KALVQOMEQLRQ 327  
  
RESULT 2  
A47141  
apolipoprotein A-IV I isoform - baboon (fragment)  
C;Species: Papio sp. (baboon)  
C;Date: 16-Feb-1994 #sequence\_revision 18-Nov-1994 #text\_change 12-Apr-1995  
C;Accession: A47141  
R;Hixson, J.E.; Kammerer, C.M.; Mott, G.E.; Britten, M.L.; Birnbaum, S.; Powers, P.K.; V  
J. Biol. Chem. 268, 15667-15673, 1993  
A;Title: Baboon apolipoprotein A-IV. Identification of Lys76-->Glu that distinguishes tw  
A;Reference number: A47141; PMID:93340170; PMID:8101842  
A;Accession: A47141  
A;Status: preliminary  
A;Molecule type: nucleic acid  
A;Residues: 1-401 <HIX>  
A;Cross-references: UNIPARC:UPI0000125BEC  
A;Experimental source: intestine  
A;Note: sequence extracted from NCBI backbone (NCBIN:136009, NCBIPI:136010)  
C;Superfamily: apolipoprotein A-I  
  
Query Match 100.0%; Score 56; DB 2; Length 401;  
Best Local Similarity 100.0%; Pred. No. 0.04;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 KALVQOMEQLRQ 12  
Db 300 KALVQOMEQLRQ 311

## RESULT 3

S29565  
apolipoprotein A-IV - crab-eating macaque  
C;Species: Macaca fascicularis (crab-eating macaque)  
C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C;Accession: S30195; S29565  
R;Osada, J.; Pocovi, M.; Nicolosi, R.J.; Schaefer, E.J.; Ordovas, J.M.  
Biochim. Biophys. Acta 1172, 335-339, 1993  
A;Title: Nucleotide sequences of the Macaca fascicularis apolipoprotein C-III and A-IV g  
A;Reference number: S30195; MUID:93192330; PMID:8448212  
A;Accession: S30195  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-429 <OSA>  
A;Cross-references: UNIPROT:P33621; UNIPARC:UPI0000125BEB; EMBL:X68361; NID:g38050; PIDN  
C;Genetics:  
A;Introns: 17/1; 59/2  
C;Superfamily: apolipoprotein A-I

Query Match 100.0%; Score 56; DB 2; Length 429;  
Best Local Similarity 100.0%; Pred. No. 0.043;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12

Db 316 KALVQOMEQLRQ 327

## RESULT 4

I54248  
apolipoprotein A-IV - chimpanzee (fragment)  
C;Species: Pan troglodytes (chimpanzee)  
C;Date: 02-Jul-1996 #sequence\_revision 02-Jul-1996 #text\_change 09-Jul-2004  
C;Accession: I54248  
R;Kamboh, M.I.; Kelly, L.J.; Ahn, Y.I.; Ferrell, R.E.  
Hum. Biol. 66, 625-638, 1994  
A;Title: Genetic polymorphism of apolipoprotein A-IV in the chimpanzee: common deletion  
A;Reference number: I54248; MUID:94374966; PMID:8088751  
A;Accession: I54248  
A;Status: preliminary; translated from GB/EMBL/DBDJ  
A;Molecule type: DNA  
A;Residues: 1-91 <RES>  
A;Cross-references: UNIPROT:Q28857; UNIPARC:UPI00000879FB; GB:S72300; NID:g601800; PIDN:  
C;Genetics:  
A;Gene: APOA4  
C;Superfamily: apolipoprotein A-I

Query Match 91.1%; Score 51; DB 2; Length 91;  
Best Local Similarity 100.0%; Pred. No. 0.065;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLR 11

Db 11 KALVQOMEQLR 21

## RESULT 5

B40892  
apolipoprotein A-IV precursor - mouse (strain 129)  
C;Species: Mus musculus (house mouse)  
C;Date: 27-Mar-1992 #sequence\_revision 10-Apr-1992 #text\_change 09-Jul-2004  
C;Accession: B40892  
R;Reue, K.; Leete, T.H.  
J. Biol. Chem. 266, 12715-12721, 1991  
A;Title: Genetic variation in mouse apolipoprotein A-IV due to insertion and deletion in  
A;Reference number: A40892; MUID:91286309; PMID:1648102  
A;Accession: B40892  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-391 <REU>  
A;Cross-references: UNIPROT:P06728; UNIPARC:UPI000016CC00; GB:M64248; NID:gl91884; PIDN:

A;Note: the authors translated the codon CTG for residue 87 as Glu, GAG for residue 207  
C;Superfamily: apolipoprotein A-I  
C;Keywords: lipid binding; lipoprotein

Query Match 87.5%; Score 49; DB 2; Length 391;  
Best Local Similarity 83.3%; Pred. No. 0.62;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12  
|||||:||||  
Db 316 KALVQOLEQFRQ 327

RESULT 6  
A40892  
apolipoprotein A-IV precursor - mouse (strain C57BL16)  
C;Species: Mus musculus (house mouse)  
C;Date: 27-Mar-1992 #sequence\_revision 10-Apr-1992 #text\_change 09-Jul-2004  
C;Accession: A40892  
R;Reue, K.; Leete, T.H.  
J. Biol. Chem. 266, 12715-12721, 1991  
A;Title: Genetic variation in mouse apolipoprotein A-IV due to insertion and deletion in  
A;Reference number: A40892; MUID:91286309; PMID:1648102  
A;Accession: A40892  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-395 <REU>  
A;Cross-references: UNIPROT:P06728; UNIPARC:UPI0000029367; GB:M64249; NID:G191886; PIDN:  
A;Note: the authors translated the codon CTG for residue 87 as Glu, GAG for residue 207  
C;Superfamily: apolipoprotein A-I  
C;Keywords: lipid binding; lipoprotein

Query Match 87.5%; Score 49; DB 2; Length 395;  
Best Local Similarity 83.3%; Pred. No. 0.63;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12  
|||||:||||  
Db 316 KALVQOLEQFRQ 327

RESULT 7  
C40892  
apolipoprotein A-IV precursor - mouse  
C;Species: Mus musculus castaneus (southeastern Asian house mouse)  
C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 31-Dec-2004  
C;Accession: C40892  
R;Reue, K.; Leete, T.H.  
J. Biol. Chem. 266, 12715-12721, 1991  
A;Title: Genetic variation in mouse apolipoprotein A-IV due to insertion and deletion in  
A;Reference number: A40892; MUID:91286309; PMID:1648102  
A;Accession: C40892  
A;Molecule type: mRNA  
A;Residues: 1-399 <REU>  
A;Cross-references: UNIPROT:Q01488; UNIPARC:UPI00001777A5; GB:M64250  
A;Note: the authors translated the codon CTG for residue 87 as Glu, GAG for residue 207  
C;Keywords: chylomicron; duplication; HDL; lipid binding; lipid transport; lipoprotein;

Query Match 87.5%; Score 49; DB 2; Length 399;  
Best Local Similarity 83.3%; Pred. No. 0.63;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12  
|||||:||||  
Db 316 KALVQOLEQFRQ 327

RESULT 8  
A25281  
apolipoprotein A-IV precursor - mouse  
C;Species: Mus musculus (house mouse)  
C;Date: 25-Oct-1987 #sequence\_revision 25-Oct-1987 #text\_change 09-Jul-2004  
C;Accession: A25281

R;Williams, S.C.; Bruckheimer, S.M.; Lusis, A.J.; LeBoeuf, R.C.; Kinniburgh, A.J.  
Mol. Cell. Biol. 6, 3807-3814, 1986  
A;Title: Mouse apolipoprotein A-IV gene: nucleotide sequence and induction by a high-lip  
A;Reference number: A25281; MUID:87089722; PMID:3796595  
A;Accession: A25281  
A;Molecule type: DNA  
A;Residues: 1-394 <WIL>  
A;Cross-references: UNIPROT:P06728; UNIPARC:UPI0000161CD8; GB:M13966; NID:G192006; PIDN:  
C;Genetics:  
A;Introns: 16/1; 58/2  
C;Superfamily: apolipoprotein A-I  
C;Keywords: chylomicron; HDL; lipid binding; lipoprotein

Query Match 78.6%; Score 44; DB 2; Length 394;  
Best Local Similarity 81.8%; Pred. No. 4.5;  
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ALVQOMEQLRQ 12  
|||||:||||  
Db 316 ALVQOLEQFRQ 326

RESULT 9  
LPRT34  
apolipoprotein A-IV precursor - rat  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 27-Nov-1985 #sequence\_revision 27-Nov-1985 #text\_change 09-Jul-2004  
C;Accession: A03095; A25214; C24700  
R;Boguski, M.S.; Elshourbagy, N.; Taylor, J.M.; Gordon, J.I.  
Proc. Natl. Acad. Sci. U.S.A. 81, 5021-5025, 1984  
A;Title: Rat apolipoprotein A-IV contains 13 tandem repetitions of a 22-amino acid segme  
A;Reference number: A03095; MUID:84298074; PMID:6591177  
A;Accession: A03095  
A;Molecule type: mRNA  
A;Residues: 1-391 <BOG>  
A;Cross-references: UNIPROT:P02651; UNIPARC:UPI0000167943; GB:M00002; GB:K02421; NID:920  
J. Biol. Chem. 261, 6398-6407, 1986  
A;Title: Evolution of the apolipoproteins. Structure of the rat APO-A-IV gene and its re  
A;Reference number: A25214; MUID:86196059; PMID:3009456  
A;Accession: A25214  
A;Molecule type: protein  
A;Residues: 1-252, 'Q', 254-391 <BO2>  
A;Cross-references: UNIPARC:UPI0000125BEE  
R;Haddad, I.A.; Ordovas, J.M.; Fitzpatrick, T.; Karathanasis, S.K.  
J. Biol. Chem. 261, 13268-13277, 1986  
A;Title: Linkage, evolution, and expression of the rat apolipoprotein A-I, C-III, and A-  
A;Reference number: A92558; MUID:87008540; PMID:3020028  
A;Accession: C24700  
A;Molecule type: DNA  
A;Residues: 1-252, 'Q', 254-391 <HAD>  
A;Cross-references: UNIPARC:UPI0000125BEE; GB:J02588; NID:G202937; PIDN:AAA40747.1; PID  
C;Comment: This apoprotein is a major component of HDL and chylomicrons but, unlike othe  
C;Comment: Nine of the thirteen 22-amino acid tandem repeats (each 22-mer is actually a  
cal, and many of these helices are amphipathic. They may therefore serve as lipid-bindin  
C;Superfamily: apolipoprotein A-I  
C;Keywords: chylomicron; duplication; HDL; lipid transport; plasma; tandem repeat  
F;1-20/Domain: signal sequence #status predicted <STG>  
F;21-391/Product: apolipoprotein A-IV #status predicted <MAT>  
F;33-330/Region: 22-residue repeats

Query Match 76.8%; Score 43; DB 1; Length 391;  
Best Local Similarity 81.8%; Pred. No. 6.6;  
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ALVQOMEQLRQ 12  
|||||:||||  
Db 317 ALVQOMEKFRQ 327

RESULT 10  
A56235  
transcription activator MafB - chicken

C;Species: Gallus gallus (chicken)  
 C;Date: 03-Oct-1995 #sequence\_revision 03-Oct-1995 #text\_change 09-Jul-2004  
 C;Accession: A56235  
 R;Kataoka, K.; Fujiwara, K.T.; Noda, M.; Nishizawa, M.  
 Mol. Cell. Biol. 14, 7581-7591, 1994  
 A;Title: MafB, a new Maf family transcription activator that can associate with Maf and  
 A;Reference number: A56235; MUID:95021288; PMID:7935473  
 A;Accession: A56235  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-311 <KAT>  
 A;Cross-references: UNIPROT:Q90888; UNIPARC:UPI00000FDAD0; GB:D28600; NID:G516723; PIDN:  
 C;Genetics:  
 A;Introns: #status absent  
 C;Superfamily: maf transforming protein; maf homology  
 C;Keywords: DNA binding; homodimer; leucine zipper  
 F;200-289/Domain: maf homology <MAF>

Query Match 69.6%; Score 39; DB 2; Length 311;  
 Best Local Similarity 70.0%; Pred. No. 26; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 3

Qy 3 LVQVMEQLRQ 12  
 Db 261 LIQVVEQLKQ 270  
 |:|:|:|:|

RESULT 11  
 J;149529  
 transcription factor-kr - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Date: 09-Mar-1996 #sequence\_revision 09-Mar-1996 #text\_change 09-Jul-2004  
 C;Accession: I49529  
 R;Cordes, S.P.; Barsh, G.S.  
 Cell 79, 1025-1034, 1994  
 A;Title: The mouse segmentation gene kr encodes a novel basic domain-leucine zipper tran  
 A;Reference number: A55200; MUID:95094266; PMID:8001130  
 A;Accession: I49529  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-323 <RES>  
 A;Cross-references: UNIPROT:P54841; UNIPARC:UPI0000002CD; GB:I36435; NID:G625043; PIDN:  
 C;Superfamily: maf transforming protein; maf homology  
 C;Keywords: leucine zipper; transcription factor  
 F;212-301/Domain: maf homology <MAF>

Query Match 69.6%; Score 39; DB 2; Length 323;  
 Best Local Similarity 70.0%; Pred. No. 27; Mismatches 0; Indels 0; Gaps 0;  
 Matches 7; Conservative 3

Qy 3 LVQVMEQLRQ 12  
 Db 273 LIQVVEQLKQ 282  
 |:|:|:|:|

RESULT 12  
 T05113  
 hypothetical protein F28M20.240 - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 09-Jul-2004  
 C;Accession: T05113  
 R;Bevan, M.; Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Hoheisel, J.; Mewes,  
 submitted to the Protein Sequence Database, November 1998  
 A;Reference number: Z15398  
 A;Accession: T05113  
 A;Molecule type: DNA  
 A;Residues: 1-2712 <BEV>  
 A;Cross-references: UNIPROT:Q9SB74; UNIPARC:UPI000009D841; EMBL:AL031004  
 A;Experimental source: cultiVar Columbia; BAC clone F28M20  
 C;Genetics:  
 A;Map position: 4  
 A;Introns: 17/3; 240/1; 1950/1; 2118/3; 2381/1; 2599/3; 2645/1; 2679/2  
 A;Note: F28M20.240

Query Match 69.6%; Score 39; DB 2; Length 2712;  
 Best Local Similarity 66.7%; Pred. No. 23e+02; Mismatches 2; Indels 0; Gaps 0;  
 Matches 8; Conservative 2

Qy 1 KALVQVMEQLRQ 12  
 Db 1873 KALVQVQDRLKQ 1884  
 |:|:|:|:|

RESULT 13  
 B41886  
 flagellar membrane protein fliz - Bacillus subtilis  
 N;Alternate names: flagellar formation protein fliz  
 C;Species: Bacillus subtilis  
 C;Date: 04-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 09-Jul-2004  
 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter  
 C;Accession: B41886; H69625  
 R;Bischoff, D.S.; Weinreich, M.D.; Ordal, G.W.  
 J. Bacteriol. 174, 4017-4025, 1992  
 A;Title: Nucleotide sequences of Bacillus subtilis flagellar biosynthetic genes fliz and  
 A;Reference number: A41886; MUID:92283757; PMID:1597417  
 A;Accession: B41886  
 A;Molecule type: DNA  
 A;Residues: 1-219 <BIS>  
 A;Cross-references: UNIPROT:P35536; UNIPARC:UPI00000603E9; GB:M87005; NID:G142928; PIDN:  
 A;Note: sequence extracted from NCBI backbone (NCBIN:106465, NCBIP:106467)  
 R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter  
 C;Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho  
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.  
 Nature 390, 249-256, 1997  
 A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler  
 tech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.  
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois  
 A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel  
 Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle  
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon,  
 A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror  
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpatra, P.; Tognoni, A.; Tosato, V.; Uchiyama,  
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yanane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.  
 A;Authors: Yoshikawa, H.P.; Zumstein, E.; Yoshikawa, H.; Danchin, A.  
 A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.  
 A;Reference number: A69580; MUID:98044033; PMID:9384377  
 A;Accession: H69625  
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-219 <KUN>  
 A;Cross-references: UNIPARC:UPI00000603E9; GB:Z99112; GB:AL009126; NID:G2633902; PIDN:CA  
 A;Experimental source: strain 168  
 C;Genetics:  
 A;Gene: fliz  
 C;Keywords: transmembrane protein

Query Match 67.9%; Score 38; DB 2; Length 219;  
 Best Local Similarity 58.3%; Pred. No. 27; Mismatches 4; Indels 0; Gaps 0;  
 Matches 7; Conservative 4

Qy 1 KALVQVMEQLRQ 12  
 Db 194 KALKEQLBELKQ 205  
 |:|:|:|:|

RESULT 14  
 S40998  
 hypothetical protein M01A8.2 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 06-Jan-1995  
 C;Accession: S40998  
 R;Hawkins, T.; Thomas, K.  
 submitted to the EMBL Data Library, October 1993  
 A;Reference number: S40997  
 A;Accession: S40998  
 A;Status: preliminary  
 A;Molecule type: DNA

A;Residues: 1-597 <HAW>  
A;Cross-references: UNIPARC:UPI000017BAC4; EMBL:Z27081  
C;Genetics:  
A;Introns: 40/3; 76/1; 125/1; 199/1; 240/1; 274/1; 292/3; 392/3; 429/2; 486/2; 521/1

Query Match 67.9%; Score 38; DB 2; Length 597;  
Best Local Similarity 66.7%; Pred. No. 73;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12  
| | | | | | | | | |  
Db 429 KILVQQIEDLR 440

RESULT 15  
G88551  
Protein M01A8.2 [imported] - Caenorhabditis elegans  
C;Species: Caenorhabditis elegans  
C;Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 09-Jul-2004  
C;Accession: G88551  
R;anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biological processes  
A;Reference number: A75000; MUID:99069613; PMID:9851916  
A;Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C\_elegans/  
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and Science 286, 1571-1577, 1999  
A;Accession: G88551  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-893 <STO>  
A;Cross-references: UNIPROT:P34531; UNIPARC:UPI000013B94B; GB:chr\_III; PIDN:CAA81607.1;  
C;Genetics:  
A;Gene: M01A8.2  
A;Map position: 3

Query Match 67.9%; Score 38; DB 2; Length 893;  
Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12  
| | | | | | | | | |  
Db 725 KILVQQIEDLR 736

RESULT 16  
B69520  
hypothetical protein AF2162 - Archaeoglobus fulgidus  
C;Species: Archaeoglobus fulgidus  
C;Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 09-Jul-2004  
C;Accession: B69520  
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson  
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.  
Nature 390, 364-370, 1997  
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiaich, P.; Kaine, B.P.; Sykes, S.  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeon  
A;Reference number: A69250; MUID:98049343; PMID:9389475  
A;Accession: B69520  
A;Status: preliminary; nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-177 <KLE>  
A;Cross-references: UNIPROT:O28120; UNIPARC:UPI0000056A4A; GB:AE000955; GB:AE000782; NID  
C;Superfamily: Archaeoglobus fulgidus hypothetical protein AP2162

Query Match 66.1%; Score 37; DB 2; Length 177;  
Best Local Similarity 58.3%; Pred. No. 32;  
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12  
| | | | | | | | | |  
Db 153 KALIPQLDALRQ 164

RESULT 17  
AI2368  
hypothetical protein alr4505 [imported] - Nostoc sp. (strain PCC 7120)  
C;Species: Nostoc sp. PCC 7120  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 09-Jul-2004  
C;Accession: AI2368  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AI2368  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-359 <KUR>  
A;Cross-references: UNIPROT:Q8YNQ7; UNIPARC:UPI000000CEB59; GB:BA000019; PIDN:BA876204.1;  
A;Experimental source: strain PCC 7120  
C;Genetics:  
A;Gene: alr4505

Query Match 66.1%; Score 37; DB 2; Length 359;  
Best Local Similarity 58.3%; Pred. No. 65;  
Matches 7; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12  
| | | | | | | | | |  
Db 210 KALYKQLEELQQ 221

RESULT 18  
AH2007  
toxin secretion ABC transporter ATP-binding protein alr1614 [imported] - Nostoc sp. (str  
C;Species: Nostoc sp. PCC 7120  
A;Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 05-Oct-2004  
C;Accession: AH2007  
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi  
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.  
DNA Res. 8, 205-213, 2001  
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana  
A;Reference number: AB1807; MUID:21595285; PMID:11759840  
A;Accession: AH2007  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-893 <KUR>  
A;Cross-references: UNIPROT:Q8YVJ9; UNIPARC:UPI000000CEI4C; GB:BA000019; PIDN:BA877980.1;  
A;Experimental source: strain PCC 7120  
C;Genetics:  
C;Superfamily: ATP dependent ABC transporter

Query Match 66.1%; Score 37; DB 2; Length 893;  
Best Local Similarity 63.6%; Pred. No. 1.6e+02;  
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ALVQOMEQLRQ 12  
| | | | | | | | | |  
Db 437 ARVQELSIQRQ 447

RESULT 19  
E75520  
hypothetical protein - Deinococcus radiodurans (strain R1)  
C;Species: Deinococcus radiodurans  
C;Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 09-Jul-2004  
C;Accession: E75520  
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;  
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;  
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.

A;Reference number: A75250; MUID:20036896; PMID:10567266  
A;Accession: E75520  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-208 <WHI>  
A;Cross-references: UNIPROT:Q9RX92; UNIPARC:UPI00000C1754; GB:AE001902; GB:AE000513; NID:  
A;Experimental source: strain R1  
C;Genetics:  
A;Gene: DR0423  
A;Map position: 1

Query Match 64.3%; Score 36; DB 2; Length 208;  
Best Local Similarity 88.9%; Pred. No. 56;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 LVQMEQLR 11  
||| |||||  
Db 157 LVQAMEQLR 165

## RESULT 20

AG0761  
probable propanol dehydrogenase (EC 1.1.1.-) [imported] - Salmonella enterica subsp. ent  
C;Species: Salmonella enterica subsp. enterica serovar Typhi  
A;Note: this species has also been called Salmonella typhi  
C;Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 31-Dec-2004  
C;Accession: AG0761  
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,  
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov  
A;Reference number: AB0502; MUID:21534947; PMID:11677608  
A;Accession: AG0761  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-370 <PAR>  
A;Cross-references: UNIPARC:UPI0000059C67; GB:AL513382; PIDN:CAD02413.1; PID:g16503282;  
C;Genetics:  
A;Gene: pduQ  
C;Superfamily: iron-containing alcohol dehydrogenase.; lactaldehyde reductase homology  
C;Keywords: oxidoreductase

Query Match 64.3%; Score 36; DB 2; Length 370;  
Best Local Similarity 63.6%; Pred. No. 1e+02;  
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ALVQMEQLRQ 12  
||:|:|:|:|:  
Db 305 ALIQIETLKQ 315

Search completed: April 14, 2006, 13:14:12  
Job time : 41 secs

GenCore version 5.1.7  
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OM protein - protein search, using sw model

Run on: April 14, 2006, 13:06:23 ; Search time 237 Seconds  
(without alignments)  
35.723 Million cell updates/sec

Title: US-09-991-809-1  
Perfect score: 56  
Sequence: 1 KALVQOMEQLRQ 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt\_05.80.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	244	2 Q13784 HUMAN	Q13784 homo sapien
2	56	100.0	396	1 APOA4 HUMAN	P06727 homo sapien
3	56	100.0	396	2 Q6Q787 HUMAN	Q6Q787 homo sapien
4	56	100.0	401	1 APOA4_FAPAN	Q28758 papio anubi
5	56	100.0	429	1 APOA4_MACFA	P33621 macaca fasc
6	51	91.1	91	2 Q28857 PANTR	Q28857 pan troglod
7	49	87.5	376	2 Q81017 MOUSE	Q81017 mus musculus
8	49	87.5	395	1 APOA4_MOUSE	P06728 mus musculus
9	49	87.5	395	2 Q91XP8 MOUSE	Q91XP8 mus musculus
10	49	87.5	395	2 Q9DBN0_MOUSE	Q9DBN0 mus musculus
11	49	87.5	435	2 Q01488 MUSMC	Q01488 mus musculus
12	47	83.9	382	1 APOA4_FIG	O46409 sus scrofa
13	43	76.8	391	1 APOA4_RAT	P02651 rattus norv
14	43	76.8	391	2 Q5BK92 RAT	Q5BK92 rattus norv
15	43	76.8	546	2 Q4KIK2_PSEF5	Q4KIK2 pseudomonas
16	41	73.2	366	2 Q6C4J9_YARLI	Q6C4J9 yarrowia li
17	41	73.2	398	2 Q8R0V5_MOUSE	Q8R0V5 mus musculus
18	41	73.2	595	2 Q9F7L4_PRR01	Q9F7L4 gamma-prote
19	41	73.2	903	2 Q6SG74_9BACT	Q6SG74 uncultured
20	41	73.2	903	2 Q6UCY3_GGAMM	Q6UCY3 uncultured
21	41	73.2	903	2 Q7BKFI_PRR01	Q7BKFI gamma-prote
22	40	71.4	221	2 Q749G9_GEOSL	Q749G9 geobacter s
23	40	71.4	313	2 Q6DE84_XENLA	Q6DE84 xenopus lae
24	40	71.4	313	2 Q9PUA6_XENLA	Q9PUA6 xenopus lae
25	40	71.4	360	2 Q8GLO8_AERSA	Q8GLO8 aeromonas s
26	40	71.4	521	2 Q561A9_CRYNE	Q561A9 cryptococcu
27	40	71.4	521	2 Q5KQ10_CRYNE	Q5KQ10 cryptococcu
28	39	69.6	138	2 Q4TVN3_SHEEP	Q4TVN3 ovnis aries
29	39	69.6	311	2 Q90370_COTJA	Q90370 coturnix co
30	39	69.6	311	2 Q90888_CHICK	Q90888 gallus gall
31	39	69.6	323	1 MAFB_HUMAN	Q9Y5Q3 homo sapien

32 39 69.6 323 1 MAFB\_MOUSE  
33 39 69.6 323 1 MAFB\_RAT  
34 39 69.6 425 2 Q5WI42\_BACSK  
35 39 69.6 460 2 Q8C459\_MOUSE  
36 39 69.6 500 2 Q72G31\_DESVH  
37 39 69.6 2712 2 Q9SB74\_ARATH  
38 38 67.9 219 1 FLIZ\_BACSU  
39 38 67.9 259 1 SRPS\_PSEPU  
40 38 67.9 259 1 TTGV\_PSEPU  
41 38 67.9 263 2 Q4R7F7\_MACFA  
42 38 67.9 306 2 Q7U5A6\_SYNXP  
43 38 67.9 369 2 Q5XHD2\_XENLA  
44 38 67.9 369 2 Q640B4\_XENLA  
45 38 67.9 482 2 Q75C16\_ASHGO

P54841 mus musculus  
P54842 rattus norv  
Q5WI42 bacillus c1  
Q8C459 mus musculus  
Q72G31 deulfovibr  
Q9SB74 arabidopsis  
P35536 bacillus su  
Q9R9U0 pseudomonas  
Q93PU6 pseudomonas  
Q4R7F7 macaca fasc  
Q7U5A6 synchococc  
Q5XHD2 xenopus lae  
Q640B4 xenopus lae  
Q75C16 ashbya goss

#### ALIGNMENTS

RESULT 1  
Q13784 HUMAN  
ID Q13784 HUMAN PRELIMINARY; PRT; 244 AA.  
AC Q13784;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE APOA4 protein (Fragment).  
GN Name=APOA4;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Liver;  
RX MEDLINE=86016704; PubMed=3931073;  
RA Karathanasis S.K.;  
RT "Apolipoprotein multigene family: tandem organization of human  
apolipoprotein AI, CIII, and AIV genes.";  
RL Proc. Natl. Acad. Sci. U.S.A. 82:6374-6378 (1985).  
DR EMBL; M10373; AAB59516.1; -; mRNA.  
DR PIR; A94137; LPHUA4.  
DR HSSP; P02649; 1B68.  
DR GO; GO:0005576; C:extracellular region; IEA.  
DR GO; GO:0008289; F:lipid binding; IEA.  
DR GO; GO:0006889; P:lipid transport; IEA.  
DR GO; GO:0042157; P:lipoprotein metabolism; IEA.  
DR InterPro; IPR000074; APOA1\_A4\_E.  
DR Pfam; PF01442; Apolipoprotein; 1.  
KW Lipoprotein.  
FT NON\_TER  
SQ SEQUENCE 244 AA; 28157 MW; 01616ACB53F12734 CRC64;

Query Match 100.0%; Score 56; DB 2; Length 244;  
Best Local Similarity 100.0%; Pred. No. 0.17;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KALVQOMEQLRQ 12  
Db 182 KALVQOMEQLRQ 193

RESULT 2  
APOA4 HUMAN  
ID APOA4 HUMAN STANDARD; PRT; 396 AA.  
AC P06727;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Apolipoprotein A-IV precursor (ApoA-IV) (ApoA-IV).  
GN Name=APOA4;  
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Intestine;  
RX MEDLINE=89194198; PubMed=2930771; DOI=10.1016/0005-2760(89)90292-0;  
RA Yang C., Gu Z.W., Xiong W., Rosseneu M., Yang H.X., Lee B.M.,  
RA Gatto A.M. Jr., Chan L.;  
RT "The primary structure of human apolipoprotein A-IV";  
RL Biochim. Biophys. Acta 1002:231-237(1989).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=87041474; PubMed=3095936;  
RA Karathanasis S.K., Oettgen P., Haddad I.A., Antonarakis S.E.;  
RT "Structure, evolution, and polymorphisms of the human apolipoprotein  
RT A4 gene (APOA4)";  
RL Proc. Natl. Acad. Sci. U.S.A. 83:8457-8461(1986).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=86296629; PubMed=3755616;  
RA Karathanasis S.K., Yunis I.;  
RT "Structure, evolution, and tissue-specific synthesis of human  
RT apolipoprotein AIV";  
RL Biochemistry 25:3962-3970(1986).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=87250378; PubMed=3036793;  
RA Elshourbagy N.A., Walker D.W., Paik Y.K., Boguski M.S., Freeman M.,  
RA Gordon J.I., Taylor J.M.;  
RT "Structure and expression of the human apolipoprotein A-IV gene";  
RL J. Biol. Chem. 262:7973-7981(1987).  
RN [5]  
RP NUCLEOTIDE SEQUENCE OF 21-396.  
RX MEDLINE=86111885; PubMed=3080432;  
RA Elshourbagy N.A., Walker D.W., Boguski M.S., Gordon J.I., Taylor J.M.;  
RT "The nucleotide and derived amino acid sequence of human  
RT apolipoprotein A-IV mRNA and the close linkage of its gene to the  
RT genes of apolipoproteins A-I and C-III";  
RL J. Biol. Chem. 261:1998-2002(1986).  
RN [6]  
RP SIGNAL SEQUENCE CLEAVAGE SITE.  
RX MEDLINE=84161950; PubMed=6706947;  
RA Gordon J.I., Bisgaier C.L., Sims H.F., Sachdev O.P., Glickman R.M.,  
RA Strauss A.W.;  
RT "Biosynthesis of human preapolipoprotein A-IV";  
RL J. Biol. Chem. 259:468-474(1984).  
RN [7]  
RP REVIEW ON POLYMORPHISM.  
RA Lohse P., Brewer H.B. Jr.;  
RT "Genetic polymorphism of apolipoprotein A-IV";  
RL Curr. Opin. Lipidol. 2:90-95(1991).  
RN [8]  
RP VARIANT A-IV\*2.  
RX MEDLINE=9027616; PubMed=2351649;  
RA Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.;  
RT "Genetic polymorphism of human plasma apolipoprotein A-IV is due to  
RT nucleotide substitutions in the apolipoprotein A-IV gene";  
RL J. Biol. Chem. 265:10061-10064(1990).  
RN [9]  
RP VARIANTS A-IV\*0 AND A-IV\*3.  
RX MEDLINE=90324273; PubMed=1973689;  
RA Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.;  
RT "Human plasma apolipoproteins A-IV-0 and A-IV-3. Molecular basis for  
RT two rare variants of apolipoprotein A-IV-1";  
RL J. Biol. Chem. 265:12734-12739(1990).  
RN [10]  
RP VARIANTS.  
RX MEDLINE=91310615; PubMed=1677358;  
RA Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.;  
RT "Three genetic variants of human plasma apolipoprotein A-IV: apoA-IV-  
RT 1 (Thr-347-->Ser), apoA-IV-0 (Lys-167-->Glu, Gln-360-->His), and apoA-IV-

RT 3 (Glu-165-->Lys)";  
RL J. Biol. Chem. 266:13513-13518(1991).  
RN [11]  
RP ERRATUM.  
RA Lohse P., Kindt M.R., Rader D.J., Brewer H.B. Jr.;  
RL J. Biol. Chem. 266:19866-19866(1991).  
RN [12]  
RP VARIANT MET-13.  
RX MEDLINE=92238494; PubMed=1349197;  
RA von Eckardstein A., Funke H., Schulte M., Erren M., Schulte H.,  
RA Asmann G.;  
RT "Nonsynonymous polymorphic sites in the apolipoprotein (apo) A-IV gene  
RT are associated with changes in the concentration of apo B- and apo A-  
RT I-containing lipoproteins in a normal population";  
RL Am. J. Hum. Genet. 50:1115-1128(1992).  
RN [13]  
RP VARIANT SER-147.  
RX MEDLINE=92144647; PubMed=1737067; DOI=10.1016/0925-4439(92)90147-F;  
RA Tenkanen H., Koskinen P., Metsä J., Baumann M., Lukka M.,  
RA Kauppinen-Makelin R., Kontula K., Taskinen M.R., Manttari M.,  
RA Manninen V., Ehnholm C.;  
RT "A novel polymorphism of apolipoprotein A-IV is the result of an  
RT asparagine to serine substitution at residue 127";  
RL Biochim. Biophys. Acta 1138:27-33(1992).  
RN [14]  
RP VARIANT A-IV\*5.  
RX MEDLINE=93138374; PubMed=1487136;  
RA Kamboh M.I., Williams E.R., Law J.C., Aston C.E., Bunker C.H.,  
RA Ferrell R.E., Pollitzer W.S.;  
RT "Molecular basis of a unique African variant (A-IV 5) of human  
RT apolipoprotein A-IV and its significance in lipid metabolism";  
RL Genet. Epidemiol. 9:379-388(1992).  
RN [15]  
RP VARIANTS BUDAPEST-2 LYS-44; BUDAPEST-1 CYS-305 AND SER-367.  
RX MEDLINE=95245341; PubMed=7728150;  
RA Menzel H.J., Dieplinger H., Sandholzer C., Karadi I., Utermann G.,  
RA Csaszar A.;  
RT "Apolipoprotein A-IV polymorphism in the Hungarian population: gene  
RT frequencies, effect on lipid levels, and sequence of two new  
RT variants";  
RL Hum. Mutat. 5:58-65(1995).  
RN [16]  
RP VARIANTS SEATTLE-3 SER-161; SEATTLE-1 LEU-178 AND SEATTLE-2 GLN-264.  
RX MEDLINE=97114287; PubMed=8956036;  
RX DOI=10.1002/(SICI)1098-1004(1996)8:4<319::AID-HUMU4>3.3.CO;2-T;  
RA Deeb S.S., Nevins D.N., Iwasaki L., Brunzell J.D.;  
RT "Two novel apolipoprotein A-IV variants in individuals with familial  
RT combined hyperlipidemia and diminished levels of lipoprotein lipase  
RT activity";  
RL Hum. Mutat. 8:319-325(1996).  
RN [17]  
RP VARIANT HIS-380.  
RX MEDLINE=99318094; PubMed=10391210; DOI=10.1038/10297;  
RA Halushka M.K., Fan J.-B., Bentley K., Hsie L., Shen N., Weder A.,  
RA Cooper R., Lipshutz R., Chakravarti A.;  
RT "Patterns of single-nucleotide polymorphisms in candidate genes for  
RT blood-pressure homeostasis";  
RL Nat. Genet. 22:239-247(1999).  
CC -!- FUNCTION: May have a role in chylomicrons and VLDL secretion and  
CC catabolism. Required for efficient activation of lipoprotein  
CC lipase by ApoC-II; potent activator of LCAT. ApoA-IV is a major  
CC component of HDL and chylomicrons.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Synthesized primarily in the intestine and  
CC secreted in plasma.  
CC -!- DOMAIN: Nine of the thirteen 22-amino acid tandem repeats (each  
CC 22-mer is actually a tandem array of two, A and B, related 11-  
CC mers) occurring in this sequence are predicted to be highly alpha-  
CC helical, and many of these helices are amphipathic. They may  
CC therefore serve as lipid-binding domains with lecithin:cholesterol  
CC acyltransferase (LCAT) activating abilities.  
CC -!- POLYMORPHISM: Eight alleles have been characterized (APOA-IV\*0 to  
CC APOA-IV\*7). APOA-IV\*1 is the major allele (90%), APOA-IV\*2 is also



CC common (8\*), the others are rare alleles.  
CC -!- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.  
CC -----  
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use as long as its content is in no way modified and this statement is not  
CC removed.  
CC -----  
CC EMBL; M14642; AAA51745.1; -; Genomic\_DNA.  
CC EMBL; X13629; CAA31955.1; -; mRNA.  
CC EMBL; M14566; AAA51748.1; -; mRNA.  
CC EMBL; J02758; AAA96731.1; -; Genomic\_DNA.  
CC EMBL; M13654; AAA51744.1; -; mRNA.  
CC PIR; A94137; LPHUA4.  
CC HSSP; P02649; 1OR2.  
CC DR SWISS-2DPAGE; P06727; HUMAN.  
CC Dr Ensembl; ENSG00000198652; Homo sapiens.  
CC HGNC; HGNC:602; APOA4.  
CC MIM; 107690; -.  
CC GO; GO:0005576; C:extracellular region; NAS.  
CC GO; GO:0005319; F:lipid transporter activity; TAS.  
CC GO; GO:0008015; P:circulation; TAS.  
CC GO; GO:0006629; P:lipid metabolism; NAS.  
CC GO; GO:0006869; F:lipid transport; TAS.  
CC InterPro; IPR000074; APOA1\_A4\_E.  
CC PANTHER; PTHR18976; APOA1\_A4\_E; 1.  
CC Pfam; PF01442; Apolipoprotein; 2.  
CC Chylomicron; HDL; Lipid transport; Plasma; Polymorphism; Repeat;  
KW Signal; Transport.  
FT SIGNAL 1 20  
FT CHAIN 21 396 Apolipoprotein A-IV.  
FT REPEAT 33 54 1.  
FT REPEAT 60 81 2.  
FT REPEAT 82 103 3.  
FT REPEAT 115 136 4.  
FT REPEAT 137 158 5.  
FT REPEAT 159 180 6.  
FT REPEAT 181 202 7.  
FT REPEAT 203 224 8.  
FT REPEAT 225 246 9.  
FT REPEAT 247 268 10.  
FT REPEAT 269 286 11.  
FT REPEAT 287 308 12.  
FT REPEAT 309 330 13.  
FT REGION 33 330 13 X 22 AA approximate tandem repeats.  
Query Match 100.0%; Score 56; DB 1; Length 396;  
Best Local Similarity 100.0%; Pred. No. 0.27;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KALVQOMEQLRQ 12  
Db 316 KALVQOMEQLRQ 327  
RESULT 3  
Q6Q787 HUMAN PRELIMINARY; PRT; 396 AA.  
AC Q6Q787;  
DT 10-MAY-2005 (TrEMBLrel. 30, Created)  
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)  
DE Apolipoprotein A-IV.  
GN Name=APOA4;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
OC Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX PubMed=15108119; DOI=10.1007/s00439-004-1106-x;

RA Fullerton S.M., Buchanan A.V., Sonpar V.A., Taylor S.L., Smith J.D.,  
RA Carlson C.S., Salomaa V., Stengard J.H., Boerwinkle E., Clark A.G.,  
RA Nickerson D.A., Weiss K.M.;  
RA "The effects of scale: variation in the APOA1/C3/A4/A5 gene cluster.";  
RL Hum. Genet. 115:36-56(2004).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Nickerson D.A., Smith J.D., Fullerton S.M., Clark A.G., Stengard J.H.,  
RA Salomaa V., Boerwinkle E., Sing C.F., Weiss K.M.;  
RA Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Brain;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,  
RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villaton D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RA "Generation and initial analysis of more than 15,000 full-length human  
RA and mouse cDNA sequences.";  
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Brain;  
RA Director MGC Project;  
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY555191; AAS68228.1; -; Genomic DNA.  
DR EMBL; AY422950; AAQ91809.1; -; Genomic DNA.  
DR EMBL; BC074764; AAH74764.1; -; mRNA.  
DR Lipoprotein.  
SQ LipoProtein. 396 AA; 45399 MW; 193753196CA2FA4A CRC64;  
Query Match 100.0%; Score 56; DB 2; Length 396;  
Best Local Similarity 100.0%; Pred. No. 0.27;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KALVQOMEQLRQ 12  
Db 316 KALVQOMEQLRQ 327  
RESULT 4  
APOA4 PAPAN STANDARD; PRT; 401 AA.  
ID APOA4 PAPAN  
AC Q28758;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Apolipoprotein A-IV precursor (Apo-AIV) (ApoA-IV) (Fragment).  
GN Name=APOA4;  
OS Papio anubis (Olive baboon).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
OC Cercopitheidae; Cercopitheinae; Papio.  
OX NCBI\_TaxID=9555;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC TISSUE=Intestine;  
RX MEDLINE=93340170; PubMed=8101842;  
RA Hixson J.E., Kammerer C.M., Mott G.E., Britten M.L., Birnbaum S.,

RA Powers P.K., Vandenberg J.L.;  
 RT "Baboon apolipoprotein A-IV. Identification of Lys-76-->Glu that  
 RT distinguishes two common isoforms and detection of length  
 RT polymorphisms at the carboxyl terminus.";  
 RL J. Biol. Chem. 268:15667-15673(1993).  
 CC -!- FUNCTION: May have a role in chylomicrons and VLDL secretion and  
 CC catabolism. Required for efficient activation of lipoprotein  
 CC lipase by ApoC-II; potent activator of LCAT. ApoA-IV is a major  
 CC component of HDL and chylomicrons.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Synthesized primarily in the intestine and  
 CC secreted in plasma.  
 CC -!- DOMAIN: Nine of the thirteen 22-amino acid tandem repeats (each  
 CC 22-mer is actually a tandem array of two, A and B, related 11-  
 CC mers) occurring in this sequence are predicted to be highly alpha-  
 CC helical, and many of these helices are amphipathic. They may  
 CC therefore serve as lipid-binding domains with lecithin:cholesterol  
 CC acyltransferase (LCAT) activating abilities.  
 CC -!- POLYMORPHISM: There are two common APOA-IV isoforms, I (shown  
 CC here) and E. The I isoform is associated with higher levels of  
 CC high density lipoprotein-C on a high cholesterol, saturated fat  
 CC diet.  
 CC -!- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.  
 CC -----  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; L13174; AAA3579.1; -; mRNA.  
 DR HSSP; P02649; 1B68.  
 DR InterPro; IPR000074; ApoA1\_A4\_E.  
 DR PANTHER; PTHR18976; ApoA1\_A4\_E; 1.  
 DR Pfam; PF01442; Apolipoprotein; 2.  
 KW Chylomicron; HDL; Lipid transport; Plasma; Polymorphism; Repeat;  
 KW Signal; Transport.  
 FT SIGNAL <1 4  
 FT CHAIN 5 401 Potential.  
 FT REPEAT 17 38 Apolipoprotein A-IV.  
 FT REPEAT 44 65 1.  
 FT REPEAT 66 87 2.  
 FT REPEAT 99 120 3.  
 FT REPEAT 121 142 4.  
 FT REPEAT 143 164 5.  
 FT REPEAT 165 186 6.  
 FT REPEAT 187 208 7.  
 FT REPEAT 209 230 8.  
 FT REPEAT 231 252 9.  
 FT REPEAT 253 270 10.  
 FT REPEAT 271 292 11.  
 FT REPEAT 293 314 12.  
 FT REGION 17 314 13 X 22 AA approximate tandem repeats.  
 FT COMPIAS 356 394 Gln/Glu-rich.  
 FT VARIANT 80 80 K -> E (in isoform E).  
 FT NON\_TER 1  
 SQ SEQUENCE 401 AA; 46538 MW; 0A76D1284AA9837F CRC64;  
 Query Match 100.0%; Score 56; DB 1; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 0.27;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KALVQOMEQLRQ 12  
 |||||  
 Db 300 KALVQOMEQLRQ 311

RESULT 5  
 APOA4 MACFA STANDARD; PRT; 429 AA.  
 AC P33621;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)  
 DE Apolipoprotein A-IV precursor (ApoA-IV) (ApoA-IV).  
 GN Name=APOA4;  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 OC Cercopitheidae; Cercopithecinae; Macaca.  
 OX NCBI\_TaxID=9541;  
 RN [1]  
 RP NUCLEOTIDE SEQUENCE.  
 RC TISSUE=Leukocyte;  
 RX MEDLINE=93192330; PubMed=8448212; DOI=10.1016/0167-4781(93)90226-4;  
 RA Osada J., Pocovi M., Nicolosi R.J., Schaefer E.J., Ordovas J.M.;  
 RT "Nucleotide sequences of the Macaca fascicularis apolipoprotein C-III  
 RT and A-IV genes.";  
 RL Biochim. Biophys. Acta 1172:335-339(1993).  
 CC -!- FUNCTION: May have a role in chylomicrons and VLDL secretion and  
 CC catabolism. Required for efficient activation of lipoprotein  
 CC lipase by ApoC-II; potent activator of LCAT. ApoA-IV is a major  
 CC component of HDL and chylomicrons.  
 CC -!- SUBCELLULAR LOCATION: Secreted.  
 CC -!- TISSUE SPECIFICITY: Secreted in plasma.  
 CC -!- DOMAIN: Nine of the thirteen 22-amino acid tandem repeats (each  
 CC 22-mer is actually a tandem array of two, A and B, related 11-  
 CC mers) occurring in this sequence are predicted to be highly alpha-  
 CC helical, and many of these helices are amphipathic. They may  
 CC therefore serve as lipid-binding domains with lecithin:cholesterol  
 CC acyltransferase (LCAT) activating abilities.  
 CC -!- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.  
 CC -----  
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 CC the European Bioinformatics Institute. There are no restrictions on its  
 CC use as long as its content is in no way modified and this statement is not  
 CC removed.  
 CC -----  
 CC EMBL; X68361; CAA48421.1; -; Genomic\_DNA.  
 DR PIR; S30195; S29565.  
 DR HSSP; P02649; 1B68.  
 DR InterPro; IPR000074; ApoA1\_A4\_E.  
 DR PANTHER; PTHR18976; ApoA1\_A4\_E; 1.  
 DR Pfam; PF01442; Apolipoprotein; 2.  
 KW Chylomicron; HDL; Lipid transport; Plasma; Repeat; Signal; Transport.  
 KW SIGNAL 1 20 By similarity.  
 FT CHAIN 21 429 Apolipoprotein A-IV.  
 FT REPEAT 33 54 1.  
 FT REPEAT 60 81 2.  
 FT REPEAT 82 103 3.  
 FT REPEAT 115 136 4.  
 FT REPEAT 137 158 5.  
 FT REPEAT 159 180 6.  
 FT REPEAT 181 202 7.  
 FT REPEAT 203 224 8.  
 FT REPEAT 225 246 9.  
 FT REPEAT 247 268 10.  
 FT REPEAT 269 286 11.  
 FT REPEAT 287 308 12.  
 FT REPEAT 309 330 13.  
 FT REGION 33 330 13 X 22 AA approximate tandem repeats.  
 FT COMPIAS 372 420 Gln/Glu-rich.  
 SQ SEQUENCE 429 AA; 49877 MW; 3D458F551D0DB60C CRC64;  
 Query Match 100.0%; Score 56; DB 1; Length 429;  
 Best Local Similarity 100.0%; Pred. No. 0.29;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KALVQOMEQLRQ 12  
 |||||  
 Db 316 KALVQOMEQLRQ 327

RESULT 6  
 Q28857\_PANTR

ID Q28857\_PANTR PRELIMINARY; PRT; 91 AA.  
AC Q28857;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE Apolipoprotein A-IV (Fragment).  
GN Name=APOA4;  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;  
OC Pan.  
OX NCBI\_TaxID=9598;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=94374966; PubMed=8088751;  
RA Kamboh M.I., Kelly L.J., Ahn Y.I., Ferrell R.E.;  
RT "Genetic polymorphism of apolipoprotein A-IV in the chimpanzee: common  
RT deletion of a conserved 12-nucleotide tandem repeat.";  
RL Hum. Biol. 66:625-638 (1994).  
DR EMBL; S72300; AAB31973.1; -; Genomic\_DNA.  
DR PIR; I54248; I54248.  
KW Lipoprotein.  
FT NON\_TER 91 91  
SQ SEQUENCE 91 AA; 10619 MW; 5D654DD84D33A4A0 CRC64;  
Query Match 91.1%; Score 51; DB 2; Length 91;  
Best Local Similarity 100.0%; Pred. No. 0.47;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 KALVQOMEQLR 11  
Db 11 KALVQOMEQLR 21  
RESULT 7  
Q81017\_MOUSE  
ID Q81017\_MOUSE PRELIMINARY; PRT; 376 AA.  
AC Q81017;  
DT 01-JUN-2003 (TREMBLrel. 24, Created)  
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)  
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
DE ApoA4 protein.  
GN Name=ApoA4;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX STRAIN=C57BL/6J; TISSUE=Embryo;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ussin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S.J., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shvchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]

RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Embryo;  
RG NIH MGC Project;  
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC050149; AAH50149.1; -, mRNA.  
DR GO; GO:0005576; C:extracellular region; IEA.  
DR GO; GO:0008289; P:lipid binding; IEA.  
DR GO; GO:0006869; P:lipid transport; IEA.  
DR GO; GO:0042157; P:lipoprotein metabolism; IEA.  
DR InterPro; IPR000074; ApoA1\_A4\_E.  
DR Pfam; PF01442; Apolipoprotein; 2.  
SQ SEQUENCE 376 AA; 42916 MW; 3B8B7EC1611D1E8B CRC64;  
Query Match 87.5%; Score 49; DB 2; Length 376;  
Best Local Similarity 83.3%; Pred. No. 4.2;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 KALVQOMEQLRQ 12  
Db 316 KALVQOMEQLRQ 327  
RESULT 8  
APOA4\_MOUSE  
ID APOA4\_MOUSE STANDARD; PRT; 395 AA.  
AC P06728;  
DT 01-JAN-1988 (Rel. 06, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Apolipoprotein A-IV precursor (Apo-AIV) (ApoA-IV).  
GN Name=ApoA4;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RX MEDLINE=87089722; PubMed=3796595;  
RA Williams S.C., Bruckheimer S.M., Lusis A.J., LeBoeuf R.C.,  
RA Kinniburgh A.J.;  
RT "Mouse apolipoprotein A-IV gene: nucleotide sequence and induction by  
RT a high-lipid diet.";  
RL Mol. Cell. Biol. 6:3807-3814 (1986).  
RN [2]  
RP SEQUENCE REVISION.  
RA Kinniburgh A.J.;  
RL Submitted (DEC-1986) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=129/J, and C57BL/6J;  
RX MEDLINE=91286309; PubMed=1648102;  
RA Reue K., Leese T.H.;  
RT "Genetic variation in mouse apolipoprotein A-IV due to insertion and  
RT deletion in a region of tandem repeats.";  
RL J. Biol. Chem. 266:12715-12721 (1991).  
CC -!- FUNCTION: May have a role in chylomicrons and VLDL secretion and  
CC catabolism. Required for efficient activation of lipoprotein  
CC lipase by ApoC-II; potent activator of LCAT. ApoA-IV is a major  
CC component of HDL and chylomicrons.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- TISSUE SPECIFICITY: Secreted in plasma.  
CC -!- DOMAIN: Nine of the thirteen 22-amino acid tandem repeats (each  
CC 22-mer is actually a tandem array of two, A and B, related 11-  
CC mers) occurring in this sequence are predicted to be highly alpha-  
CC helical, and many of these helices are amphipathic. They may  
CC therefore serve as lipid-binding domains with lectin:cholesterol  
CC acyltransferase (LCAT) activating abilities.  
CC -!- POLYMORPHISM: There is a polymorphism within a series of imperfect  
CC repeats encoding the sequence E-Q-[AV]-Q. Insertions or deletions  
CC of 12 nucleotides have given rise to three forms characterized by  
CC three (129), four (C57BL/6), or five (M.castaneus) copies of the  
CC repeat unit.

```
CC      -!- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
DR      EMBL; M1366; AAA37253.1; -; Genomic_DNA.
DR      EMBL; M64249; AAA37215.1; -; mRNA.
DR      EMBL; M64248; AAA37214.1; -; mRNA.
DR      PIR; A25281; A25281.
DR      PIR; A40892; A40892.
DR      PIR; B40892; B40892.
DR      Ensembl; ENSMUSG00000032080; Mus musculus.
DR      MGI; MGI:88051; ApoA4.
DR      GO; GO:0005615; C:extracellular space; TAS.
DR      GO; GO:0030300; P:regulation of cholesterol absorption; IMP.
DR      InterPro; IPR000074; ApoA1_A4_E.
DR      PANTHER; PTHR18976; ApoA1_A4_E.1.
DR      Pfam; PF01442; Apolipoprotein_2.
KW      Chylomicron; HDL; Lipid transport; Plasma; Polymorphism; Repeat;
KW      Signal; Transport.
FT      SIGNAL          1      20
FT      CHAIN           21      395  Apolipoprotein A-IV.
FT      REPEAT          33      54  1.
FT      REPEAT          60      81  2.
FT      REPEAT          82     103  3.
FT      REPEAT         115     136  4.
FT      REPEAT         137     158  5.
FT      REPEAT         159     180  6.
FT      REPEAT         181     202  7.
FT      REPEAT         203     224  8.
FT      REPEAT         225     246  9.
FT      REPEAT         247     268  10.
FT      REPEAT         269     286  11.
FT      REPEAT         287     308  12.
FT      REPEAT         309     330  13.
FT      REGION          33      330  13 X 22 AA approximate tandem repeats.
FT      COMPBias        366     389  Gln/Glu-rich.
FT      VARIANT         382     385  Missing (in some strains).
FT      CONFLICT        15      15  Missing (in Ref. 1).
FT      CONFLICT        63      63  Q -> K (in Ref. 1).
FT      CONFLICT        207     207  E -> R (in Ref. 1).
FT      CONFLICT        288     288  S -> A (in Ref. 1).
FT      CONFLICT        294     295  RQ -> KA (in Ref. 1).
FT      CONFLICT        315     316  NK -> GG (in Ref. 1).
FT      CONFLICT        315     316
SQ      SEQUENCE        395 AA; 45029 MW; 5FE27D0236226257 CRC64;

Query Match      87.5%; Score 49; DB 1; Length 395;
Best Local Similarity 83.3%; Pred. No. 4.4;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KALVQMEQLRQ 12
Db      316 KALVQLEQFRQ 327
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RESULT 9
Q91XF8 MOUSE PRELIMINARY; PRT; 395 AA.
AC      Q91XF8
ID      Q91XF8
DT      01-DEC-2001 (TrEMBLrel. 19, Created)
DT      01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      ApoA4 protein.
GN      Name=ApoA4;
OS      Mus musculus (Mouse)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]

Query Match      87.5%; Score 49; DB 2; Length 395;
Best Local Similarity 83.3%; Pred. No. 4.4;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KALVQMEQLRQ 12
Db      316 KALVQLEQFRQ 327
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RESULT 10
Q9DBN0 MOUSE PRELIMINARY; PRT; 395 AA.
AC      Q9DBN0
ID      Q9DBN0
DT      01-JUN-2001 (TrEMBLrel. 17, Created)
DT      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Mus musculus adult male liver cDNA, RIKEN full-length enriched
DE      library, clone:130002K10 product:apolipoprotein A-IV, full insert
DE      sequence.
GN      Name=ApoA4;
OS      Mus musculus (Mouse)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]

NUCLEOTIDE SEQUENCE
STRAIN=FVB/N; TISSUE=Kidney;
MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U.,
Schnerch A., Schein J.E., Jones S.J.M., Maizumi M.A.,
"Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]

NUCLEOTIDE SEQUENCE
STRAIN=FVB/N; TISSUE=Kidney;
Strausberg R.; to the EMBL/GenBank/DBJ databases.
Submitted (JUL-2001)
EMBL; BC010769; AAH10769.1; -; mRNA.
MGI; MGI:88051; ApoA4.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0030300; P:regulation of cholesterol absorption; IMP.
InterPro; IPR000074; ApoA1_A4_E.
Pfam; PF01442; Apolipoprotein_2.
SQ      SEQUENCE        395 AA; 45029 MW; C48BE32BED441F71 CRC64;

Query Match      87.5%; Score 49; DB 2; Length 395;
Best Local Similarity 83.3%; Pred. No. 4.4;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 KALVQMEQLRQ 12
Db      316 KALVQLEQFRQ 327
|||||:|||||

RESULT 10
Q9DBN0 MOUSE PRELIMINARY; PRT; 395 AA.
AC      Q9DBN0
ID      Q9DBN0
DT      01-JUN-2001 (TrEMBLrel. 17, Created)
DT      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Mus musculus adult male liver cDNA, RIKEN full-length enriched
DE      library, clone:130002K10 product:apolipoprotein A-IV, full insert
DE      sequence.
GN      Name=ApoA4;
OS      Mus musculus (Mouse)
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC      Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]

NUCLEOTIDE SEQUENCE
STRAIN=C57BL/6J; TISSUE=Liver;
MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.,
"High-efficiency full-length cDNA cloning."
Meth. Enzymol. 303:19-44(1999).
[2]

NUCLEOTIDE SEQUENCE
STRAIN=C57BL/6J; TISSUE=Liver;
MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
```

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Glessi C., King B., Kochiwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,  
RA Hayashizaki Y.;  
RA "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
RN [3]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RA The FANTOM Consortium,  
RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
RT "Analysis of the mouse transcriptome based on functional annotation of  
60,770 full-length cDNAs.";  
RL Nature 420:563-573(2002).  
RN [4]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;  
RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
prepare full-length cDNA libraries for rapid discovery of new genes.";  
RL Genome Res. 10:1617-1630(2000).  
RN [5]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;  
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
RA Konno H., Akiyama J., Nishi K., Kitsuai T., Tashiro H., Itoh M.,  
RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
RA Fujiwaki S., Inoue K., Togawa Y., Izawa M., Ohara E., Watahiki M.,  
RA Yoneda Y., Iehikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,  
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;  
RT "RIKEN integrated sequence analysis (RISA) system-384-format  
sequencing pipeline with 384 multicapillary sequencer.";  
RL Genome Res. 10:1757-1771(2000).  
RN [6]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=C57BL/6J; TISSUE=Liver;  
RA Adachi J., Aizawa K., Akahira S., Akimura T., Arai A., Aono H.,  
RA Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,  
RA Hanagaki T., Hara A., Hayatsu N., Hiramoto K., Hiraoka T., Hori F.,  
RA Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,  
RA Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,  
RA Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,  
RA Okazaki Y., Okido T., Owa C., Saito H., Saito R., Sakai C., Sakai K.,  
RA Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,  
RA Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,  
RA Tejima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,  
RA Muramatsu M., Hayashizaki Y.;  
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK004856; BAB23620.1; -; mRNA.  
DR MGI; MGI:88051; Apoa4.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR GO; GO:0030300; P:regulation of cholesterol absorption; IMP.  
DR InterPro; IPR000074; ApoA1\_A4\_E.  
DR Pfam; PF01442; Apolipoprotein; 2.  
KW Lipoprotein.  
SQ SEQUENCE 395 AA; 45044 MW; 4102D84ACB0D182A CRC64;

Query Match 87.5%; Score 49; DB 2; Length 395;  
Best Local Similarity 83.3%; Pred. NO. 4.4;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KALVQOMEQLRQ 12  
|||||:|||||  
DB 316 KALVQOLEQFRQ 327  
RESULT 11  
Q01488 MUSMC PRELIMINARY; PRT; 435 AA.  
ID Q01488;  
AC Q01488;  
DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Apolipoprotein A-IV precursor.  
GN Name=Apoa4; Synonyms=apoa-4;  
OS Mus musculus castaneus (Southeastern Asian house mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10091;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=CAST/BIJ; TISSUE=Liver;  
RX MEDLINE=91286309; PubMed=1648102;  
RA Reue K., Leete T.H.;  
RT "Genetic variation in mouse apolipoprotein A-IV due to insertion and  
deletion in a region of tandem repeats.";  
RL J. Biol. Chem. 266:12715-12721(1991).  
DR EMBL; M64250; AAA37216.1; -; mRNA.  
DR PIR; C40892; C40892.  
DR MGI; MGI:88051; Apoa4.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR GO; GO:0030300; P:regulation of cholesterol absorption; IMP.  
DR InterPro; IPR000074; ApoA1\_A4\_E.  
DR Pfam; PF01442; Apolipoprotein; 2.  
KW Lipoprotein; Signal.  
FT SIGNAL 1 20 Potential.  
FT CHAIN 21 435 apolipoprotein A-IV.  
SQ SEQUENCE 435 AA; 49254 MW; B2AF55EEA8E456B2 CRC64;  
Query Match 87.5%; Score 49; DB 2; Length 435;  
Best Local Similarity 83.3%; Pred. NO. 4.8;  
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
QY 1 KALVQOMEQLRQ 12  
|||||:|||||  
DB 316 KALVQOLEQFRQ 327  
RESULT 12  
APOA4\_PIG STANDARD; PRT; 382 AA.  
ID APOA4\_PIG  
AC O46409;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 10-MAY-2005 (Rel. 47, Last annotation update)  
DE Apolipoprotein A-IV precursor (ApoA-IV).  
GN Name=APOA4;  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
OC Sus.  
OX NCBI\_TaxID=9823;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA Osada J., Iturralde M., Calleja L., Gonzalez N., Pineiro A.;  
RL Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.  
CC -!- FUNCTION: May have a role in chylomicrons and VLDL secretion and  
catabolism. Required for efficient activation of lipoprotein

lipase by ApoC-II; potent activator of LCAT. ApoA-IV is a major component of HDL and chylomicrons.

!- SUBCELLULAR LOCATION: Secreted.

!- TISSUE SPECIFICITY: Secreted in plasma.

!- DOMAIN: Nine of the thirteen 22-amino acid tandem repeats (each 22-mer is actually a tandem array of two, A and B, related 11-mers) occurring in this sequence are predicted to be highly alpha-helical, and many of these helices are amphipathic. They may therefore serve as lipid-binding domains with lecithin:cholesterol acyltransferase (LCAT) activating abilities.

!- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.

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EMBL; AJ222966; CAA11020.1; -; mRNA.

HSSP; P12851; 1E23.

InterPro; IPR000074; ApoA1\_A4\_E.

PANTHER; PTHR18976; ApoA1\_A4\_E; 1.

Pfam; PF01442; Apolipoprotein; 2.

Chylomicron; HDL; Lipid transport; Plasma; Repeat; Signal; Transport.

FT SIGNAL 1 20 By similarity.

FT CHAIN 21 382 Apolipoprotein A-IV.

FT REPEAT 33 54 1.

FT REPEAT 60 81 2.

FT REPEAT 82 103 3.

FT REPEAT 115 136 4.

FT REPEAT 137 158 5.

FT REPEAT 159 180 6.

FT REPEAT 181 202 7.

FT REPEAT 203 224 8.

FT REPEAT 225 246 9.

FT REPEAT 247 268 10.

FT REPEAT 269 286 11.

FT REPEAT 287 308 12.

FT REPEAT 309 330 13.

FT REGION 33 330 13 X 22 AA approximate tandem repeats.

FT COMPIAS 360 377 Gln/Glu-rich.

FT SEQUENCE 382 AA; 43294 MW; 2AC8A9A02D4379EF CRC64;

Query Match 83.9%; Score 47; DB 1; Length 382;

Best Local Similarity 83.3%; Pred. No. 9.4;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KALVQOMEQLRQ 12

DB 316 KALVQQVEDLRQ 327

RESULT 13

APOA4 RAT STANDARD; PRT; 391 AA.

AC P02651;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Apolipoprotein A-IV precursor (Apo-AIV) (ApoA-IV).

GN Name=ApoA4;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridea; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=86196059; PubMed=3009456;

RA Boguski M.S., Birkenmeier E.H., Eshourbagy N.A., Taylor J.M., Gordon J.I.;

RT "Evolution of the apolipoproteins. Structure of the rat apo-A-IV gene and its relationship to the human genes for apo-A-I, C-III, and E.";

J. Biol. Chem. 261:6398-6407(1986).

[2]

RN NUCLEOTIDE SEQUENCE.

RP MEDLINE=84298074; PubMed=6591177;

RX Boguski M.S., Eshourbagy N.A., Taylor J.M., Gordon J.I.;

RT "Rat apolipoprotein A-IV contains 13 tandem repetitions of a 22-amino acid segment with amphipathic helical potential.";

RL Proc. Natl. Acad. Sci. U.S.A. 81:5021-5025(1984).

[3]

RN NUCLEOTIDE SEQUENCE.

RP MEDLINE=87008540; PubMed=3020028;

RX Haddad I.A., Ordovas J.M., Fitzpatrick T., Karathanasis S.K.;

RT "Linkage, evolution, and expression of the rat apolipoprotein A-I, C-III, and A-IV genes.";

RL J. Biol. Chem. 261:13268-13277(1986).

CC !- FUNCTION: May have a role in chylomicrons and VLDL secretion and catabolism. Required for efficient activation of lipoprotein lipase by ApoC-II; potent activator of LCAT. ApoA-IV is a major component of HDL and chylomicrons.

CC !- SUBCELLULAR LOCATION: Secreted.

CC !- TISSUE SPECIFICITY: Secreted in plasma.

CC !- DOMAIN: Nine of the thirteen 22-amino acid tandem repeats (each 22-mer is actually a tandem array of two, A and B, related 11-mers) occurring in this sequence are predicted to be highly alpha-helical, and many of these helices are amphipathic. They may therefore serve as lipid-binding domains with lecithin:cholesterol acyltransferase (LCAT) activating abilities.

CC !- SIMILARITY: Belongs to the apolipoprotein A1/A4/E family.

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EMBL; M00002; AAA85909.1; -; mRNA.

EMBL; J02588; AAA40747.1; -; Genomic DNA.

EMBL; M13508; AAA40748.1; -; Genomic DNA.

PIR; A03095; LPRTA4.

RGD; 2132; ApoA4.

GO; GO:0006889; P:lipid transport; TAS.

InterPro; IPR000074; ApoA1\_A4\_E.

PANTHER; PTHR18976; ApoA1\_A4\_E; 1.

Pfam; PF01442; Apolipoprotein; 2.

Chylomicron; HDL; Lipid transport; Plasma; Repeat; Signal; Transport.

FT SIGNAL 1 20

FT CHAIN 21 391 Apolipoprotein A-IV.

FT REPEAT 33 54 1.

FT REPEAT 60 81 2.

FT REPEAT 82 103 3.

FT REPEAT 115 136 4.

FT REPEAT 137 158 5.

FT REPEAT 159 180 6.

FT REPEAT 181 202 7.

FT REPEAT 203 224 8.

FT REPEAT 225 246 9.

FT REPEAT 247 268 10.

FT REPEAT 269 286 11.

FT REPEAT 287 308 12.

FT REPEAT 309 330 13.

FT REGION 33 330 13 X 22 AA approximate tandem repeats.

FT COMPIAS 374 385 Gln/Glu-rich.

FT VARIANT 253 253 Q -> H.

FT SEQUENCE 391 AA; 44456 MW; 24095004A809201D CRC64;

Query Match 76.8%; Score 43; DB 1; Length 391;

Best Local Similarity 81.8%; Pred. No. 48;

Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 ALVQOMEQLRQ 12

DB 317 ALVQOMEKFRQ 327

```
RESULT 14
Q5BK92 RAT PRELIMINARY; PRT; 391 AA.
ID Q5BK92
AC Q5BK92
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Apolipoprotein A-IV.
GN Name=ApoA4;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.2426038999;
RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullihy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Schmutz J., Myers R.M.,
RA Rodriguez A.C., Grimwood J., Green E.D., Dickson M.C.,
RA Buterfield V.S.N., Krawinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
*RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RG NIH MGC Project;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC091159; AAH91159.1; -; mRNA.
KW Lipoprotein.
SQ SEQUENCE 391 AA; 44456 MW; 24095004A809201D CRC64;

Query Match 76.8%; Score 43; DB 2; Length 391;
Best Local Similarity 81.8%; Pred. No. 48;
Matches 9; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 ALVQMQEQLRQ 12
| | | | | | | |
Db 317 ALVQMQEKFQ 327

RESULT 15
Q4KIK2 PSEF5
ID Q4KIK2 PSEF5 PRELIMINARY; PRT; 546 AA.
AC Q4KIK2;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Membrane protein, putative.
GN ORFNames=PFL_0794;
OS Pseudomonas fluorescens (strain Pf-5).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=220664;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=PF-5;
```

```
RX PubMed=15980861; DOI=10.1038/nbt1110;
RA Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S.,
RA Mavrodi D., DeBoy R.T., Seshadri R., Ren Q., Madupu R.J.,
RA Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz M.,
RA Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran K.,
RA Khouri H.M., Pierson E., Pierson L., III, Thomashow L., Loper J.,
RT "Complete genome sequence of the plant commensal Pseudomonas
RT fluorescens Pf-5.";
RL Nat. Biotechnol. 23:873-878(2005).
DR EMBL; CP000076; AAY96196.1; -; Genomic DNA.
SQ SEQUENCE 546 AA; 61305 MW; 7C3578A5906BA8A2 CRC64;

Query Match 76.8%; Score 43; DB 2; Length 546;
Best Local Similarity 75.0%; Pred. No. 66;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KALVQMQEQLRQ 12
| | | | | | | |
Db 448 KAFVSQVEQLRQ 459

RESULT 16
Q6C4J9 YARLI
ID Q6C4J9_YARLI PRELIMINARY; PRT; 366 AA.
AC Q6C4J9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to tr|CAD70383|Neurospora crassa B17B1.010.
GN OrderedLocustNames=YALIOE261479;
OS Yarrowia lipolytica (Candida lipolytica).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Dipodascaceae; Yarrowia.
OX NCBI_TaxID=4952;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., March C., Neuveglise C., Talla E.,
RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boismare A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantreya F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,
RA Nicaud J.-M., Nikolski M., Oztas S., Oxier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekai F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RN Nature 430:35-44(2004)
DR EMBL; CR382131; CAG80014.1; -; Genomic_DNA.
DR InterPro; IPR003169; GYF.
DR Pfam; PF02213; GYF; 1.
DR SMART; SM00444; GYF; 1.
DR PROSITE; PS00829; GYF; 1.
KW Complete proteome.
SQ SEQUENCE 366 AA; 41775 MW; B099A46276AA54CA CRC64;

Query Match 73.2%; Score 41; DB 2; Length 366;
Best Local Similarity 66.7%; Pred. No. 1e+02;
Matches 8; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KALVQMQEQLRQ 12
| | | | | | | |
Db 257 KAMVQQIEQLTE 268

RESULT 17
Q8ROV5_MOUSE
ID Q8ROV5_MOUSE PRELIMINARY; PRT; 398 AA.
```

AC Q8R0V5;  
DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein C230043N17Rik.  
GN Name=C230043N17Rik;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;  
OC Muridae; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=FVB/N; TISSUE=Liver;  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
RA Roak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fanev J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
● and mouse cDNA sequences.";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=FVB/N; TISSUE=Liver;  
RA Strausberg R.;  
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC026393; AAH26393.1; -; mRNA.  
DR Ensembl; ENSMUSG00000031549; Mus musculus.  
DR MGI; MGI:2142489; C230043N17Rik.  
DR GO; GO:0020037; F:heme binding; IEA.  
DR InterPro; IPR000898; Indolamine\_d0ase.  
DR Pfam; PF01231; IDO; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 398 AA; 44439 MW; 7871CCE86FE24D1A CRC64;  
  
Query Match 73.2%; Score 41; DB 2; Length 398;  
Best Local Similarity 75.0%; Pred. No. 1.1e+02;  
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
Qy 1 KALVQOMEQLRQ 12  
Db 176 KALVQGMELRQ 187  
||||| :||  
||| :||  
RESULT 18  
Q9F7L4 PRB01  
ID Q9F7L4 PRB01 PRELIMINARY; PRT; 595 AA.  
AC Q9F7L4\_ PRB01  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DE Predicted preprotein translocase secA subunit.  
DE Gamma-proteobacterium EBAC31A08.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; environmental samples.  
OX NCBI\_TaxID=133804;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RC STRAIN=20446260; PubMed=10988064; DOI=10.1126/science.289.5486.1902;  
RX MEDLINE=20446260; PubMed=10988064; DOI=10.1126/science.289.5486.1902;  
RA Beja O., Aravind L., Koonin E.V., Suzuki M.T., Hadd A., Nguyen L.P.,

RA Jovanovich S.B., Gates C.M., Feldman R.A., Spudich J.L., Spudich E.N.,  
RA DeLong E.F.;  
RT "Bacterial rhodopsin: evidence for a new type of phototrophy in the  
sea.";  
RL Science 289:1902-1906 (2000).  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Beja O., Aravind L., Koonin E.V., Suzuki M.T., Hadd A., Nguyen L.P.,  
RA Jovanovich S.B., Gates C.M., Feldman R.A., DeLong E.F.;  
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.  
CC -!- SUBUNIT: Part of the prokaryotic protein translocation apparatus  
CC which comprise secA, secB, secD, secE, secF, secG and secY (By  
CC similarity).  
DR EMBL; AF279106; AAG10505.2; -; Genomic\_DNA.  
DR HSSP; O05885; 1NKT.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004386; F:helicase activity; IEA.  
DR GO; GO:0003676; F:nucleic acid binding; IEA.  
DR GO; GO:0005515; F:protein binding; IEA.  
DR GO; GO:0017038; P:protein import; IEA.  
DR GO; GO:0006605; P:protein targeting; IEA.  
DR InterPro; IPR001650; Helicase\_C.  
DR InterPro; IPR00185; SecA.  
DR InterPro; IPR011130; SecA\_PP\_bind.  
DR InterPro; IPR011116; SecA\_SW.  
DR Pfam; PF00271; Helicase\_C\_1.  
DR Pfam; PF01043; SecA\_PP\_Bind; 1.  
DR Pfam; PF07516; SecA\_SW; 1.  
DR PRINTS; PR00906; SECA.  
DR PROSITE; PS01312; SECA; 1.  
SQ SEQUENCE 595 AA; 68004 MW; 05E1A1AF84E5BBAF CRC64;  
  
Query Match 73.2%; Score 41; DB 2; Length 595;  
Best Local Similarity 58.3%; Pred. No. 1.6e+02;  
Matches 7; Conservative 5; Mismatches 0; Indels 0; Gaps 0;  
  
Qy 1 KALVQOMEQLRQ 12  
Db 130 KALIEIEQLRK 141  
||| :|||  
||| :|||  
RESULT 19  
Q6SG74 9BACT  
ID Q6SG74\_9BACT PRELIMINARY; PRT; 903 AA.  
AC Q6SG74;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Preprotein translocase, SecA subunit.  
GN Name=secA, ORFNames=EBAC000-45B06.3;  
OS uncultured bacterium 562.  
OX Bacteria; environmental samples.  
OX NCBI\_TaxID=257397;  
RN [1]  
RP NUCLEOTIDE SEQUENCE.  
RA DeLong E.F.;  
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP NUCLEOTIDE SEQUENCE.  
RA Heidelberg J.F., Eisen J.A., Nelson W.C., DeLong E.F.;  
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AY458644; AAR37988.1; -; Genomic\_DNA.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005524; F:ATP binding; IEA.  
DR GO; GO:0004386; F:helicase activity; IEA.  
DR GO; GO:0003676; F:nucleic acid binding; IEA.  
DR GO; GO:0005515; F:protein binding; IEA.  
DR GO; GO:0017038; P:protein import; IEA.  
DR GO; GO:0006605; P:protein targeting; IEA.  
DR InterPro; IPR001650; Helicase\_C.  
DR InterPro; IPR00185; SecA.  
DR InterPro; IPR011115; SecA\_DEAD.



```
DR InterPro; IPR011130; SecA_PP_bind.
DR InterPro; IPR011116; SecA_SW.
DR Pfam; PF00271; Helicase_C; 1.
DR Pfam; PF07517; SecA_DEAD; 1.
DR Pfam; PF01043; SecA_PP_bind; 1.
DR Pfam; PF07516; SecA_SW; 1.
DR PRINTS; PR00906; SECA.
DR TIGRFAMs; TIGR00963; secA; 1.
DR PROSITE; PS01312; SECA; 1.
SQ SEQUENCE 903 AA; 102698 MW; C86A897DA3C88B4A CRC64;

Query Match      73.2%; Score 41; DB 2; Length 903;
Best Local Similarity 58.3%; Pred. No. 2.4e+02;
Matches 7; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 KALVQMEQLRQ 12
   |||:::|
Db 438 KALIEIEQLRK 449

RESULT 20
Q6UCY3_9GAMM
AC Q6UCY3_9GAMM PRELIMINARY; PRT; 903 AA.
DT 05-JUL-2004 (TRENBLrel. 27, Created)
DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
DE Predicted preprotein translocase subunit SecA.
GN ORFNames=EB000-45B06.03;
OS uncultured marine gamma proteobacterium EB000-45B06.
OC Bacteria; Proteobacteria; Gammaproteobacteria; environmental samples.
OX NCBI_TaxID=248050;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22946209; PubMed=14566056; DOI=10.1073/pnas.2133554100;
RA De la Torre J.R., Christianson L.M., Beja O., Suzuki M.T., Karl D.M.,
RA Heidelberg J.F., DeLong E.F.;
RT "Proteorhodopsin genes are distributed among divergent marine
  bacterial taxa.";
RL proc. Natl. Acad. Sci. U.S.A. 100:12830-12835(2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA de la Torre J.R., Christianson L.M., Beja O., Suzuki M.T., Karl D.M.,
RA Heidelberg J.F., DeLong E.F.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY372454; AAR05257.1; -; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004386; F:helicase activity; IEA.
DR GO; GO:0003676; F:nucleic acid binding; IEA.
DR GO; GO:0005515; F:protein binding; IEA.
DR GO; GO:0017038; P:protein import; IEA.
DR GO; GO:0006605; P:protein targeting; IEA.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR000185; SecA.
DR InterPro; IPR011115; SecA_DEAD.
DR InterPro; IPR011130; SecA_PP_bind.
DR InterPro; IPR011116; SecA_SW.
DR Pfam; PF00271; Helicase_C; 1.
DR Pfam; PF07517; SecA_DEAD; 1.
DR Pfam; PF01043; SecA_PP_bind; 1.
DR Pfam; PF07516; SecA_SW; 1.
DR PRINTS; PR00906; SECA.
DR TIGRFAMs; TIGR00963; secA; 1.
DR PROSITE; PS01312; SECA; 1.
SQ SEQUENCE 903 AA; 102698 MW; C86A897DA3C88B4A CRC64;

Query Match      73.2%; Score 41; DB 2; Length 903;
Best Local Similarity 58.3%; Pred. No. 2.4e+02;
Matches 7; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

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Db 438 KALIEIEQLRK 449
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Db 438 KALIEIEQLRK 449

Search completed: April 14, 2006, 13:13:28  
Job time : 240 secs

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